

Figure 1. Construction of a pC5 H6p WNV *prM-M-E* donor plasmid, pDS-2946-1-1

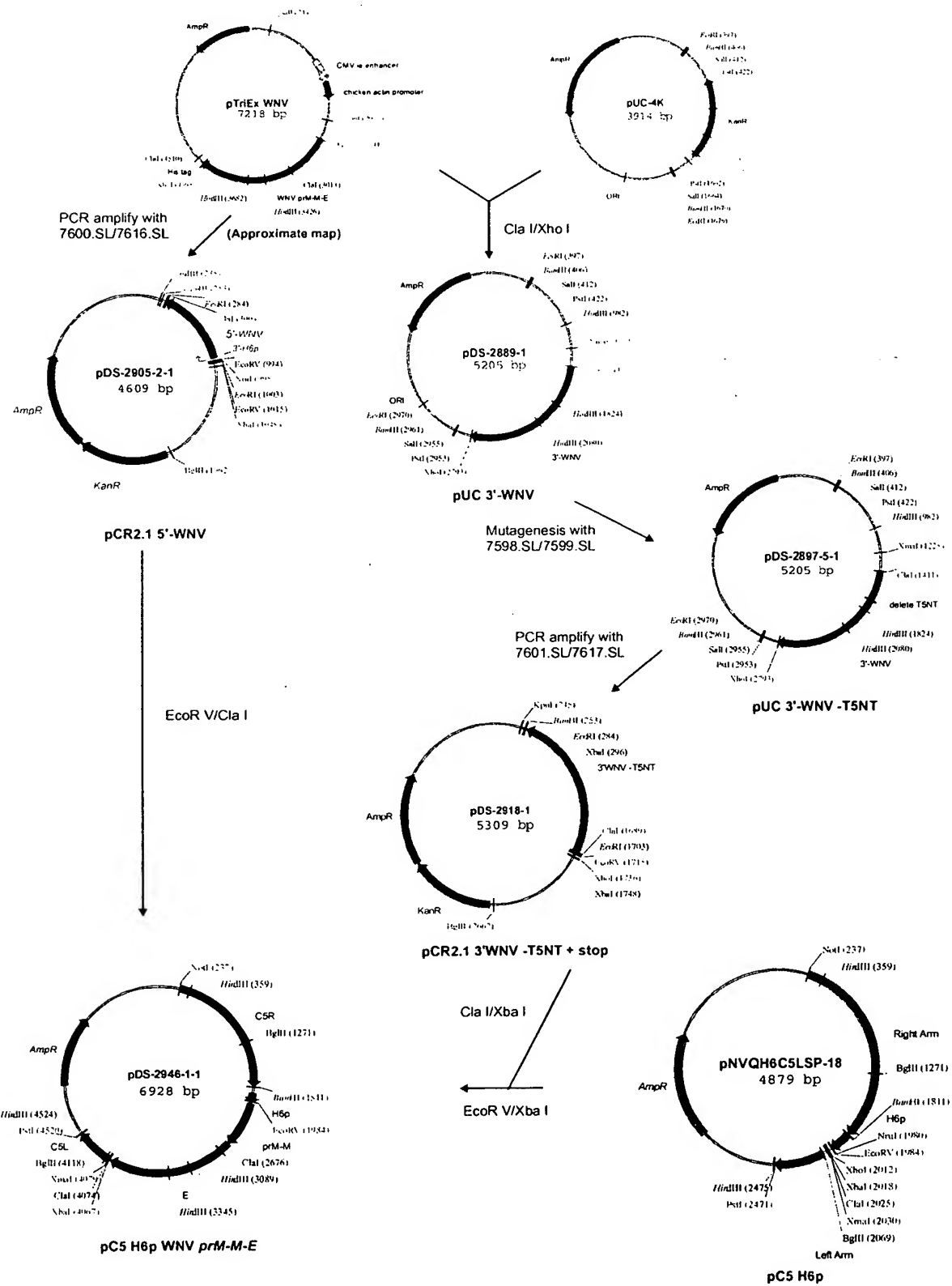


Figure 2. Sequence of C5 H6p WNV *prM-M-E* C5 in pDS-2646-1-1

⇒C5R

1 TGAATGTTAA ATGTTATACT TTGGATGAAG CTATAAATAT GCATTGGAAA AATAATCCAT

61 TTAAAGAAAG GATTCAAATA CTACAAAACC TAAGCGATAA TATGTTAACT AAGCTTATTC

121 TTAACGACGC TTTAAATATA CACAAATAAA CATAATTTTT GTATAACCTA ACAAATAACT

181 AAAACATAAA AATAATAAAA GGAAATGTAA TATCGTAATT ATTTTACTCA GGAATGGGGT

241 TAAATATTTA TATCACGTGT ATATCTATAC TGTTATCGTA TACTCTTTAC AATTACTATT

301 ACGAATATGC AAGAGATAAT AAGATTACGT ATTTAAGAGA ATCTTGTCAT GATAATTGGG

361 TACGACATAG TGATAAATGC TATTTTCGCAT CGTTACATAA AGTCAGTTGG AAAGATGGAT

421 TTGACAGATG TAACTTAATA GGTGCAAAAA TGTTAAATAA CAGCATTCTA TCGGAAGATA

481 GGATACCAGT TATATTATAC AAAAATCACT GGTGGGATAA AACAGATTCT GCAATATTCG

541 TAAAAGATGA AGATTACTGC GAATTTGTAA ACTATGACAA TAAAAAGCCA TTTATCTCAA

601 CGACATCGTG TAATTCTTCC ATGTTTTATG TATGTGTTTC AGATATTATG AGATTACTAT

661 AAACTTTTTG TATACTTATA TTCCGTAAAC TATATTAATC ATGAAGAAAA TGAAAAAGTA

721 TAGAAGCTGT TCACGAGCGG TTGTTGAAAA CAACAAAATT ATACATTCAA GATGGCTTAC

781 ATATACGTCT GTGAGGCTAT CATGGATAAT GACAATGCAT CTCTAAATAG GTTTTTGGAC

841 AATGGATTCTG ACCCTAACAC GGAATATGGT ACTCTACAAT CTCCTCTTGA AATGGCTGTA

901 ATGTTCAAGA ATACCGAGGC TATAAAAATC TTGATGAGGT ATGGAGCTAA ACCTGTAGTT

961 ACTGAATGCA CAACTTCTTG TCTGCATGAT GCGGTGTTGA GAGACGACTA CAAAATAGTG

1021 AAAGATCTGT TGAAGAATAA CTATGTAAAC AATGTTCTTT ACAGCGGAGG CTTTACTCCT

1081 TTGTGTTTGG CAGCTTACCT TAACAAAGTT AATTTGGTTA AACTTCTATT GGCTCATTCTG

1141 GCGGATGTAG ATATTTCAAA CACGGATCGG TTAACCTCTC TACATATAGC CGTATCAAAT

1201 AAAAATTTAA CAATGGTTAA ACTTCTATTG AACAAAGGTG CTGATACTGA CTTGCTGGAT

1261 AACATGGGAC GTACTCCTTT AATGATCGCT GTACAATCTG GAAATATTGA AATATGTAGC

1321 ACACTACTTA AAAAAAATAA AATGTCCAGA ACTGGGAAAA ATTGATCTTG CCAGCTGTAA

1381 TTCATGGTAG AAAAGAAGTG CTCAGGCTAC TTTTCAACAA AGGAGCAGAT GTAAACTACA

1441 TCTTTGAAAG AAATGGAAAA TCATATACTG TTTTGGAATT GATTAAAGAA AGTTACTCTG

1501 AGACACAAAA GAGGTAGCTG AAGTGGTACT CTCAAAAAGG TACGTGACTA ATTAGCTATA

1561 AAAAGGATCC GGGTTAATTA ATTAGTCATC AGGCAGGGCG AGAACGAGAC TATCTGCTCG

⇒ H6p

1621 TTAATTAATT AGAGCTTCTT TATTCTATAC TTAAAAAGTG AAAATAAATA CAAAGGTTCT

1681 TGAGGGTTGT GTTAAATTGA AAGCGAGAAA TAATCATAAA TTATTTTCATT ATCGCGATAT

⇒ WNV capsid leader

M T G I A V M I G L I A S V

1741 CCGTTAAGTT TGTATCGTAA TGACCGGAAT TGCAGTCATG ATTGGCCTGA TCGCCAGCGT

⇒ WNV prM

1801 . G A V T L S N F Q G K V M M T V N A T D .
 AGGAGCAGTT ACCCTCTCTA ACTTCCAAGG GAAGGTGATG ATGACGGTAA ATGCTACTGA

1861 . V T D V I T I P T A A G K N L C I V R A .
 CGTCACAGAT GTCATCACGA TTCCAACAGC TGCTGGAAAG AACCTATGCA TTGTCAGAGC

1921 . M D V G Y M C D D T I T Y E C P V L S A .
 AATGGATGTG GGATACATGT GCGATGATAC TATCACTTAT GAATGCCAG TGCTGTGGC

1981 . G N D P E D I D C W C T K S A V Y V R Y .
 TGGTAATGAT CCAGAAGACA TCGACTGTTG GTGCACAAAG TCAGCAGTCT ACGTCAGGTA

⇒ WNV M

2041 . G R C T K T R H S R R S R R S L T V Q T .
 TGGAAGATGC ACCAAGACAC GCCACTCAAG ACGCAGTCGG AGGTCACTGA CAGTGCAGAC

2101 . H G E S T L A N K K G A W M D S T K A T .
 ACACGGAGAA AGCACTCTAG CGAACAAGAA GGGGGCTTGG ATGGACAGCA CCAAGGCCAC

2161 . R Y L V K T E S W I L R N P G Y A L V A .
 AAGGTATTTG GTAAAAACAG AATCATGGAT CTTGAGGAAC CCTGGATATG CCCTGGTGGC

2221 . A V I G W M L G S N T M Q R V V F V V L .
 AGCCGTCATT GGTGGATGC TTGGGAGCAA CACCATGCAG AGAGTTGTGT TTGTCGTGCT

⇒ WNV E

2281 . L L L V A P A Y S F N C L G M S N R D F .
 ATTGCTTTTG GTGGCCCCAG CTTACAGCTT CAACTGCCTT GGAATGAGCA ACAGAGACTT

2341 . L E G V S G A T W V D L V L E G D S C V .
 CTTGGAAGGA GTGTCTGGAG CAACATGGGT GGATTGGTT CTCGAAGGCG ACAGCTGCGT

2401 . T I M S K D K P T I D V K M M N M E A A .
 GACTATCATG TCTAAGGACA AGCCTACCAT CGATGTGAAG ATGATGAATA TGGAGGCGGC

2461 . N L A E V R S Y C Y L A T V S D L S T K .
 CAACCTGGCA GAGGTCCGCA GTTATTGCTA TTTGGCTACC GTCAGCGATC TCTCCACCAA

2521 . A A C P T M G E A H N D K R A D P A F V .
 AGCTGCGTGC CCGACCATGG GAGAAGCTCA CAATGACAAA CGTGCTGACC CAGCTTTTGT

2581 . C R Q G V V D R G W G N G C G L F G K G .
 GTGCAGACAA GGAGTGGTGG ACAGGGGCTG GGGCAACGGC TGCGGACTAT TTGGCAAAGG

2641 . S I D T C A K F A C S T K A I G R T I L .
 AAGCATTGAC ACATGCGCCA AATTTGCCTG CTCTACCAAG GCAATAGGAA GAACCATCTT

mutated T5NT

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2701  . K E N   I K Y E   V A I   F V H   G P T T   V E S   .
      GAAAGAGAAT ATCAAGTACG AAGTGGCCAT CTTCGTGCAC GGACCAACTA CTGTGGAGTC

2761  . H G N   Y S T Q   V G A   T Q A   G R F S   I T P   .
      GCACGGAAAC TACTCCACAC AGGTTGGAGC CACTCAGGCA GGGAGATTCA GCATCACTCC

2821  . A A P   S Y T L   K L G   E Y G   E V T V   D C E   .
      TGCGGCGCCT TCATACACAC TAAAGCTTGG AGAATATGGA GAGGTGACAG TGGACTGTGA

2881  . P R S   G I D T   N A Y   Y V M   T V G T   K T F   .
      ACCACGGTCA GGGATTGACA CCAATGCATA CTACGTGATG ACTGTTGGAA CAAAGACGTT

2941  . L V H   R E W F   M D L   N L P   W S S A   G S T   .
      CTTGGTCCAT CGTGAGTGGT TCATGGACCT CAACCTCCCT TGGAGCAGTG CTGGAAGTAC

3001  . V W R   N R E T   L M E   F E E   P H A T   K Q S   .
      TGTGTGGAGG AACAGAGAGA CGTTAATGGA GTTTGAGGAA CCACACGCCA CGAAGCAGTC

3061  . V I A   L G S Q   E G A   L H Q   A L A G   A I P   .
      TGTGATAGCA TTGGGCTCAC AAGAGGGAGC TCTGCATCAA GCTTTGGCTG GAGCCATTCC

3121  . V E F   S S N T   V K L   T S G   H L K C   R V K   .
      TGTGGAATTT TCAAGCAACA CTGTCAAGTT GACGTCGGGT CATTTGAAGT GTAGAGTGAA

3181  . M E K   L Q L K   G T T   Y G V   C S K A   F K F   .
      GATGGA AAAA TTGCAGTTGA AGGGAACAAC CTATGGCGTC TGTTCAAAGG CTTTCAAGTT

3241  . L G T   P A D T   G H G   T V V   L E L Q   Y T G   .
      TCTTGGGACT CCCGCAGACA CAGGTCACGG CACTGTGGTG TTGGAATTGC AGTACACTGG

3301  . T D G   P C K V   P I S   S A A   S L N D   L T P   .
      CACGGATGGA CCTTGCAAAG TTCCTATCTC GTCAGCGGCT TCATTGAACG ACCTAACGCC

3361  . V G R   L V T V   N P F   V S V   A T A N   A K V   .
      AGTGGGCAGA TTGGTCACTG TCAACCCTTT TGTTCAGTG GCCACGGCCA ACGCTAAGGT

3421  . L I E   L E P P   F G D   S Y I   V V G R   G E Q   .
      CCTGATTGAA TTGGAACCAC CCTTTGGAGA CTCATACATA GTGGTGGGCA GAGGAGAACA

3481  . Q I N   H H W H   K S G   S S I   G K A F   T T T   .
      ACAGATCAAT CACCATTGGC ACAAGTCTGG AAGCAGCATT GGCAAAGCCT TTACAACCAC

3541  . L K G   A Q R L   A A L   G D T   A W D F   G S V   .
      CCTCAAAGGA GCGCAGAGAC TAGCCGCTCT AGGAGACACA GCTTGGGACT TTGGATCAGT

3601  . G G V   F T S V   G K A   V H Q   V F G G   A F R   .
      TGGAGGGGTG TTCACCTCAG TTGGGAAGGC TGTCCATCAA GTGTTCGGAG GAGCATTCCG

3661  . S L F   G G M S   W I T   Q G L   L G A L   L L W   .
      CTCACTGTTC GGAGGCATGT CCTGGATAAC GCAAGGATTG CTGGGGGCTC TCCTGTTGTG

3721  . M G I   N A R D   R S I   A L T   F L A V   G G V   .
      GATGGGCATC AATGCTCGTG ATAGGTCCAT AGCTCTCACG TTTCTCGCAG TTGGAGGAGT

3781  . L L F   L S V N   V H A
      TCTGCTCTTC CTCTCCGTGA ACGTGCACGC TTAATTTTTTA TCTAGAATCG ATCCCGGGTT

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⇒ C5L

3841 TTTATGACTA GTTAATCACG GCCGCCTTAT AAAGATCTAA AATGCATAAT TTCTAAATAA
3901 TGAAAAAAG TACATCATGA GCAACGCGTT AGTATATTTT ACAATGGAGA TTAACGCTCT
3961 ATACCGTTCT ATGTTTATTG ATTCAGATGA TGTTTGTAGAA AAGAAAGTTA TTGAATATGA
4021 AAACTTTAAT GAAGATGAAG ATGACGACGA TGATTATTGT TGTAATCTG TTTTAGATGA
4081 AGAAGATGAC GCGCTAAAGT ATACTATGGT TACAAAGTAT AAGTCTATAC TACTAATGGC
4141 GACTTGTGCA AGAAGGTATA GTATAGTGAA AATGTTGTTA GATTATGATT ATGAAAAACC
4201 AAATAAATCA GATCCATATC TAAAGGTATC TCCTTTGCAC ATAATTTTCAT CTATTCCTAG
4261 TTTAGAATAC

Figure 3: Construction of a pF8 H6p WNV *prM-M-E* donor plasmid, pSL-5513-1'-1-1.

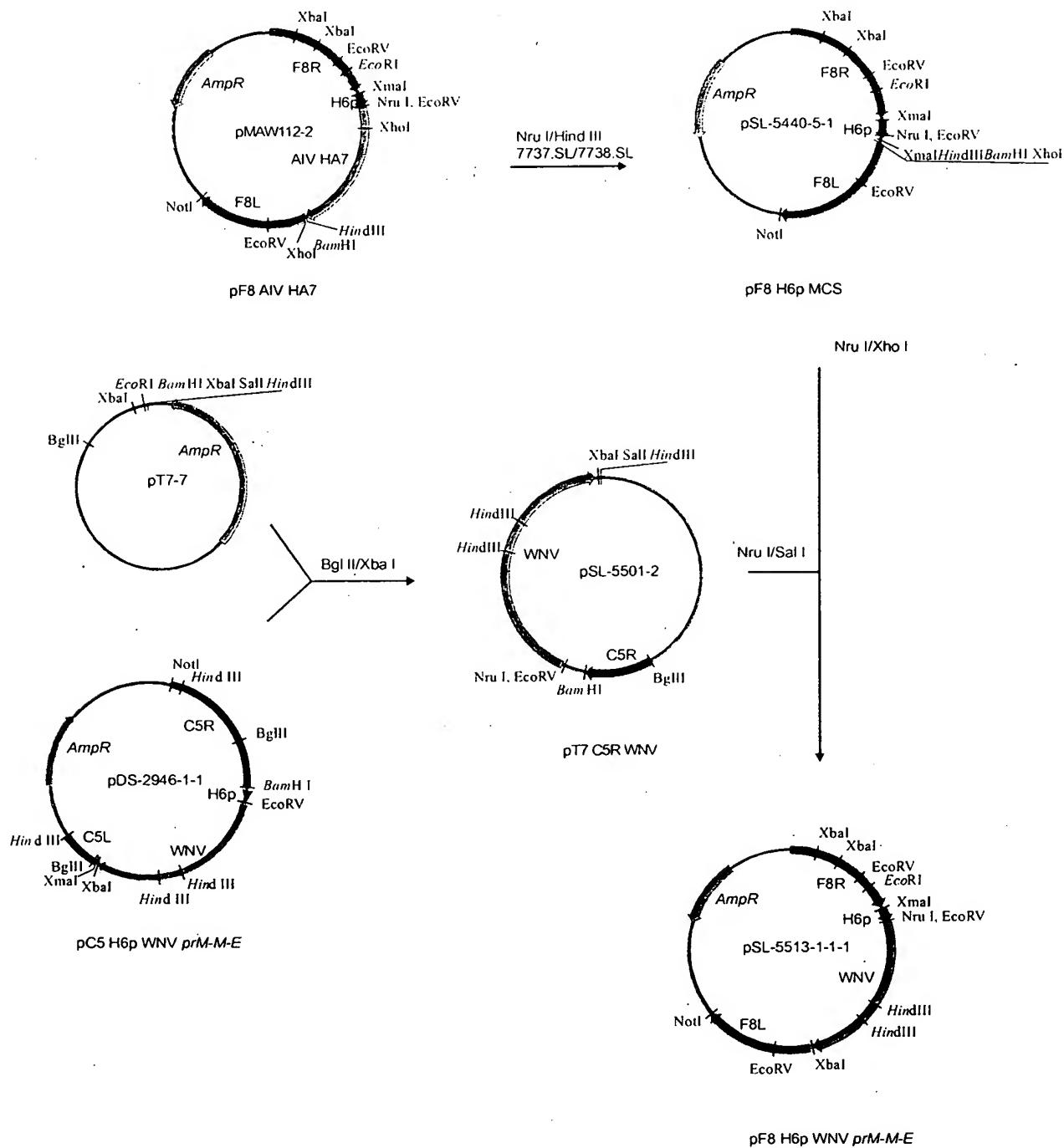


Figure 4. Sequence of F8 H6p WNV prM-M-E F8 in pSL-5513-1-1-1.

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⇒ F8R
1  GACCCCTTTAC AAGAATAAAA GAAGAAACAA CTGTGAAATA GTTTATAAAT GTAATTCGTA
61  TGCAGAAAAC GATAATATAT TTTGGTATGA GAAATCTAAA GGAGACATAG TTTGTATAGA
121 CATGCGCTCT TCCGATGAGA TATTCGATGC TTTTCTAATG TATCATATAG CTACAAGATA
181 TGCCTATCAT GATGATGATA TATATCTACA AATAGTGTTA TATTATTCTA ATAATCAAAA
241 TGTATATCT TATATTACGA AAAATAAATA CGTTAAGTAT ATAAGAAATA AACTAGAGA
301 CGATATTCAT AAAGTAAAAA TATTAGCTCT AGAAGACTTT ACAACGGAAG AAATATATTG
361 TTGGATTAGT AATATATAAC AGCGTAGCTG CACGGTTTTG ATCATTTCCT AACAATATAA
421 ACCAATGAAG GAGGACGACT CATCAAACAT AAATAACATT CACGGAAAAAT ATTCAGTATC
481 AGATTTATCA CAAGATGATT ATGTTATTGA ATGTATAGAC GGATCTTTTG ATTCGATCAA
541 GTATAGAGAT ATAAAGGTGA TAATAATGAA GAATAACGGT TACGTTAATT GTAGTAAATT
601 ATGTAAAATG CGGAATAAAT ACTTTTCTAG ATGGTTGCGT CTTTCTACTT CTAAAGCATT
661 ATTAGACATT TACAATAATA AGTCAGTAGA TAATGCTATT GTTAAAGTCT ATGGTAAAGG
721 TAAGAAACTT ATTATAACAG GATTTTATCT CAAACAAAAT ATGATACGTT ATGTTATTGA
781 GTGGATAGGG GATGATTTTA CAAACGATAT ATACAAAATG ATTAATTTCT ATAATGCGTT
841 ATTCGGTAAC GATGAATTAA AAATAGTATC CTGTGAAAAC ACTCTATGCC CGTTTATAGA
901 ACTTGGTAGA TGCTATTATG GTAAAAAATG TAAGTATATA CACGGAGATC AATGTGATAT
961 CTGTGGTCTA TATATACTAC ACCCTACCGA TATTAACCAA CGAGTTTCTC ACAAGAAAAC
1021 TTGTTTAGTA GATAGAGATT CTTTGATTGT GTTTAAAGA AGTACCAGTA AAAAGTGTGG
1081 CATATGCATA GAAGAAATAA ACAAAAAACA TATTTCCGAA CAGTATTTTG GAATTCTCCC
1141 AAGTTGTAAA CATATTTTTT GCCTATCATG TATAAGACGT TGGGCAGATA CTACCAGAAA
1201 TACAGATACT GAAAATACGT GTCCTGAATG TAGAATAGTT TTTCTTTTCA TAATACCCAG
1261 TAGGTATTGG ATAGATAATA AATATGATAA AAAAATATTA TATAATAGAT ATAAGAAAAT
1321 GATTTTTTACA AAAATACCTA TAAGAACAAT AAAAATATAA TTACATTTAC GGAAAATAGC
1381 TGGTTTTAGT TTACCAACTT AGAGTAATTA TCATATTGAA TCTATATTGC TAATTAGCTA
1441 ATAAAAACCC GGGTTAATTA ATTAGTCATC AGGCAGGGCG AGAACGAGAC TATCTGCTCG

⇒ H6p
1501 TTAATTAATT AGAGCTTCTT TATTCTATAC TTAAAAAGTG AAAATAAATA CAAAGGTTCT

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1561 TGAGGGTTGT GTTAAATTGA AAGCGAGAAA TAATCATAAA TTATTTTCATT ATCGCGATAT

⇒ WNV capsid leader

1621 CCGTTAAGTT TGTATCGTAA TGACCGGAAT TGCAGTCATG ATTGGCCTGA TCGCCAGCGT

⇒ WNV prM

1681 . G A V T L S N F Q G K V M M T V N A T D .
AGGAGCGGTT ACCCTCTCTA ACTTCCAAGG GAAGGTGATG ATGACGGTAA ATGCTACTGA

1741 . V T D V I T I P T A A G K N L C I V R A .
CGTCACAGAT GTCATCACGA TTCCAACAGC TGCTGGAAG AACCTATGCA TTGTGAGAGC

1801 . M D V G Y M C D D T I T Y E C P V L S A .
AATGGATGTG GGATACATGT GCGATGATAC TATCACTTAT GAATGCCCAG TGCTGTCCGC

1861 . G N D P E D I D C W C T K S A V Y V R Y .
TGGTAATGAT CCAGAAGACA TCGACTGTTG GTGCACAAAG TCAGCAGTCT ACGTCAGGTA

⇒ WNV M

1921 . G R C T K T R H S R R S R R S L T V Q T .
TGGAAGATGC ACCAAGACAC GCCACTCAAG ACGCAGTCGG AGGTCACTGA CAGTGCAGAC

1981 . H G E S T L A N K K G A W M D S T K A T .
ACACGGAGAA AGCACTCTAG CGAACAAGAA GGGGGCTTGG ATGGACAGCA CCAAGGCCAC

2041 . R Y L V K T E S W I L R N P G Y A L V A .
AAGGTATTTG GTAAAAACAG AATCATGGAT CTTGAGGAAC CCTGGATATG CCCTGGTGGC

2101 . A V I G W M L G S N T M Q R V V F V V L .
AGCCGTCATT GGTGGATGC TTGGGAGCAA CACCATGCAG AGAGTTGTGT TTGTCGTGCT

⇒ WNV E

2161 . L L L V A P A Y S F N C L G M S N R D F .
ATTGCTTTTG GTGGCCCCAG CTTACAGCTT CAACTGCCTT GGAATGAGCA ACAGAGACTT

2221 . L E G V S G A T W V D L V L E G D S C V .
CTTGAAGGA GTGTCTGGAG CAACATGGGT GGATTGTTGTT CTCGAAGGCG ACAGCTGCGT

2281 . T I M S K D K P T I D V K M M N M E A A .
GACTATCATG TCTAAGGACA AGCCTACCAT CGATGTGAAG ATGATGAATA TGGAGGCGGC

2341 . N L A E V R S Y C Y L A T V S D L S T K .
CAACCTGGCA GAGGTCCGCA GTTATTGCTA TTTGGCTACC GTCAGCGATC TCTCCACCAA

2401 . A A C P T M G E A H N D K R A D P A F V .
AGCTGCGTGC CCGACCATGG GAGAAGCTCA CAATGACAAA CGTGCTGACC CAGCTTTTGT

2461 . C R Q G V V D R G W G N G C G L F G K G .
GTGCAGACAA GGAGTGGTGG ACAGGGGCTG GGGCAACGGC TGCGGACTAT TTGGCAAAGG

2521 . S I D T C A K F A C S T K A I G R T I L .
AAGCATTGAC ACATGCGCCA AATTTGCCTG CTCTACCAAG GCAATAGGAA GAACCATCTT

2581 . K E N I K Y E V A I F V H G P T T V E S .
GAAAGAGAAT ATCAAGTACG AAGTGGCCAT CTTCTGTCAC GGACCAACTA CTGTGGAGTC

2641 . H G N Y S T Q V G A T Q A G R F S I T P .
 GCACGGAAAC TACTCCACAC AGGTTGGAGC CACTCAGGCA GGGAGATTCA GCATCACTCC

2701 . A A P S Y T L K L G E Y G E V T V D C E .
 TGCGGCGCCT TCATACACAC TAAAGCTTGG AGAATATGGA GAGGTGACAG TGGACTGTGA

2761 . P R S G I D T N A Y Y V M T V G T K T F .
 ACCACGGTCA GGGATTGACA CCAATGCATA CTACGTGATG ACTGTTGGAA CAAAGACGTT

2821 . L V H R E W F M D L N L P W S S A G S T .
 CTTGGTCCAT CGTGAGTGGT TCATGGACCT CAACCTCCCT TGGAGCAGTG CTGGAAGTAC

2881 . V W R N R E T L M E F E E P H A T K Q S .
 TGTGTGGAGG AACAGAGAGA CGTTAATGGA GTTTGAGGAA CCACACGCCA CGAAGCAGTC

2941 . V I A L G S Q E G A L H Q A L A G A I P .
 TGTGATAGCA TTGGGCTCAC AAGAGGGAGC TCTGCATCAA GCTTTGGCTG GAGCCATTCC

3001 . V E F S S N T V K L T S G H L K C R V K .
 TGTGGAATTT TCAAGCAACA CTGTCAAGTT GACGTCGGGT CATTGAAGT GTAGAGTGAA

3061 . M E K L Q L K G T T Y G V C S K A F K F .
 GATGGAAGAAA TTGCAGTTGA AGGGAACAAC CTATGGCGTC TGTTCAAAGG CTTTCAAGTT

3121 . L G T P A D T G H G T V V L E L Q Y T G .
 TCTTGGGACT CCCGCAGACA CAGGTCACGG CACTGTGGTG TTGGAATTGC AGTACACTGG

3181 . T D G P C K V P I S S A A S L N D L T P .
 CACGGATGGA CCTTGCAAAG TTCCTATCTC GTCAGCGGCT TCATTGAACG ACCTAACGCC

3241 . V G R L V T V N P F V S V A T A N A K V .
 AGTGGGCAGA TTGGTCACTG TCAACCCTTT TGTTCAGTG GCCACGGCCA ACGCTAAGGT

3301 . L I E L E P P F G D S Y I V V G R G E Q .
 CCTGATTGAA TTGGAACCAC CCTTTGGAGA CTCATACATA GTGGTGGGCA GAGGAGAACA

3361 . Q I N H H W H K S G S S I G K A F T T T .
 ACAGATCAAT CACCATTGGC ACAAGTCTGG AAGCAGCATT GGCAAAGCCT TTACAACCAC

3421 . L K G A Q R L A A L G D T A W D F G S V .
 CCTCAAAGGA GCGCAGAGAC TAGCCGCTCT AGGAGACACA GCTTGGGACT TTGGATCAGT

3481 . G G V F T S V G K A V H Q V F G G A F R .
 TGGAGGGGTG TTCACCTCAG TTGGGAAGGC TGTCCATCAA GTGTTGCGAG GAGCATTCCG

3541 . S L F G G M S W I T Q G L L G A L L L W .
 CTCACTGTTC GGAGGCATGT CCTGGATAAC GCAAGGATTG CTGGGGGCTC TCCTGTTGTG

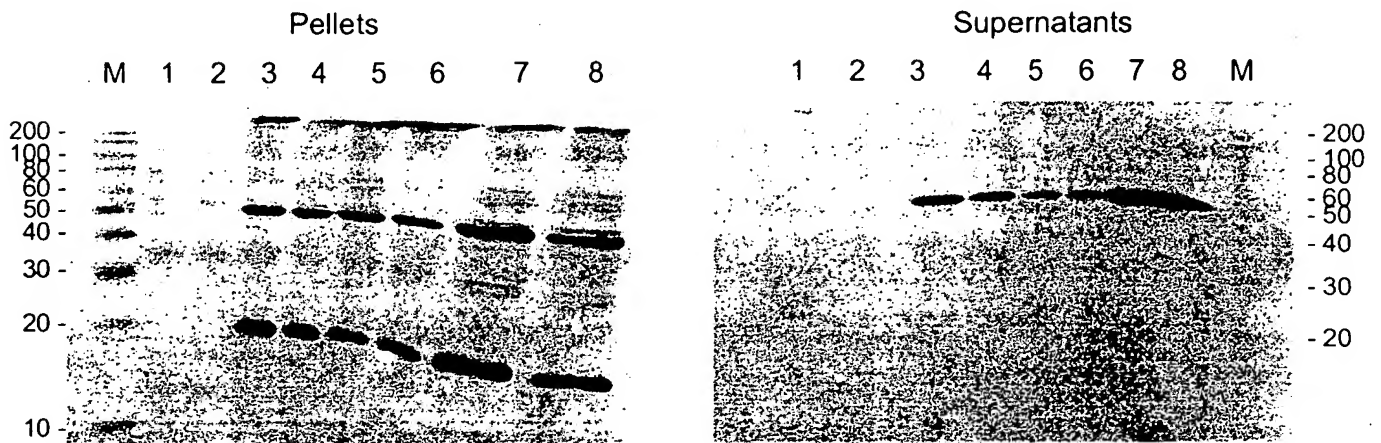
3601 . M G I N A R D R S I A L T F L A V G G V .
 GATGGGCATC AATGCTCGTG ATAGGTCCAT AGCTCTCACG TTTCTCGCAG TTGGAGGAGT

3661 . L L F L S V N V H A
 TCTGCTCTTC CTCTCCGTGA ACGTGCACGC TTAATTTTTA TCTAGAGTCG AGTTTTTATT

⇒ F8L

3721 GACTAGTTAA TCATAAGATA AATAATATAC AGCATTGTAA CCATCGTCAT CCGTTATACG
3781 GGGAAATAATA TTACCATACA GTATTATTAA ATTTTCTTAC GAAGAATATA GATCGGTATT
3841 TATCGTTAGT TTATTTTACA TTTATTAATT AAACATGTCT ACTATTACCT GTTATGGAAA
3901 TGACAAATTT AGTTATATAA TTTATGATAA AATTAAGATA ATAATAATGA AATCAAATAA
3961 TTATGTAAAT GCTACTAGAT TATGTGAATT ACGAGGAAGA AAGTTTACGA ACTGGAAAAA
4021 ATTAAGTGAA TCTAAAATAT TAGTCGATAA TGTAACAAAA ATAAATGATA AACTAACCA
4081 GTTAAAAACG GATATGATTA TATACGTAA GGATATTGAT CATAAAGGAA GAGATACTTG
4141 CGGTTACTAT GTACACCAAG ATCTGGTATC TTCTATATCA AATTGGATAT CTCCGTTATT
4201 CGCCGTTAAG GTAAATAAAA TTATTAACTA TTATATATGT AATGAATATG ATATACGACT
4261 TAGCGAAATG GAATCTGATA TGACAGAAGT AATAGATGTA GTTGATAAAT TAGTAGGAGG
4321 ATACAATGAT GAAATAGCAG AAATAATATA TTTGTTTAAT AAATTTATAG AAAAATATAT
4381 TGCTAACATA TCGTTATCAA CTGAATTATC TAGTATATTA AATAATTTTA TAAATTTTAA
4441 TAAAAAATAC AATAACGACA TAAAAGATAT TAAATCTTTA ATTCTTGATC TGAAAAACAC
4501 ATCTATAAAA CTAGATAAAA AGTTATTCGA TAAAGATAAT AATGAATCGA ACGATGAAAA
4561 ATTGGAAACA GAAGTTGATA AGCTAATTTT TTTCATCTAA ATAGTATTAT TTTATTGAAG
4621 TACGAAGTTT TACGTTAGAT AAATAATAAA GGTGATTTT TACTTTGTTA AATATCAAAT
4681 ATGTCATTAT CTGATAAAGA TACAAAAACA CACGGTGATT ATCAACCATC TAACGAACAG
4741 ATATTACAAA AAATACGTCG GACTATGGAA AACGAAGCTG ATAGCCTCAA TAGAAGAAGC
4801 ATTAAAGAAA TTGTTGTAGA TGTTATGAAG AATTGGGATC ATCCTCTCAA CGAAGAAATA
4861 GATAAAGTTC TAAACTGGAA AAATGATACA TTAAACGATT TAGATCATCT AAATACAGAT
4921 GATAATATTA AGGAAATCAT ACAATGTCTG ATTAGAGAAT TTGCGTTTAA AAAGATCAAT
4981 TCTATTATGT ATAGTTATGC TATGGTAAAA CTCAATTCAG ATAACGAAAC ATTGAAAGAT
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5101 CCATTACCC

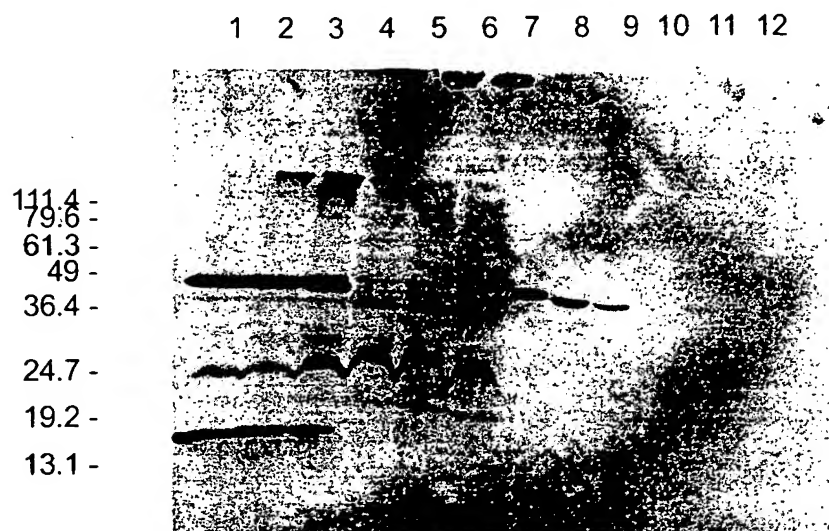
Figure 5. Immunoblot analysis of the expression of WNV proteins from pox recombinants in CEFs



Lane 1: ALVAC
 Lane 2: Fowlpox
 Lane 3: vCP2017 24h harvest
 Lane 4: vCP2017 48h harvest
 Lane 5: vCP2018 24h harvest
 Lane 6: vCP2018 48h harvest
 Lane 7: vFP2000 24h harvest
 Lane 8: vFP2000 48h harvest

vCP2017 = ALVAC WNV *prM-M-E*
 vCP2018 = ALVAC-2 WNV *prM-M-E*
 vFP2000 = Fowlpox WNV *prM-M-E*

Figure 6. Immunoblot analysis of the expression of WNV proteins from pox recombinants in BHK cells



Lane 1: vFP2000.3.2.1.2.1 pellet
 Lane 2: vCP2017.3.3 pellet
 Lane 3: vCP2018.6.3.3.2 pellet
 Lane 4: mock infected BHK pellet
 Lane 5: pTriEx-WNV transfection pellet
 Lane 6: mock transfected BHK pellet
 Lane 7: vFP2000.3.2.1.2.1 supt
 Lane 8: vCP2017.3.3 supt
 Lane 9: vCP2018.6.3.3.2 supt
 Lane 10: mock infected BHK supt
 Lane 11: pTriEx-WNV transfection supt
 Lane 12: mock transfection supt

vCP2017 = ALVAC WNV
 vCP2018 = ALVAC-2 WNV
 vFP2000 = Fowlpox WNV

Figure 7. Construction of pVR1012 WNV *prM-M-E*, pSL-5448-1-1.

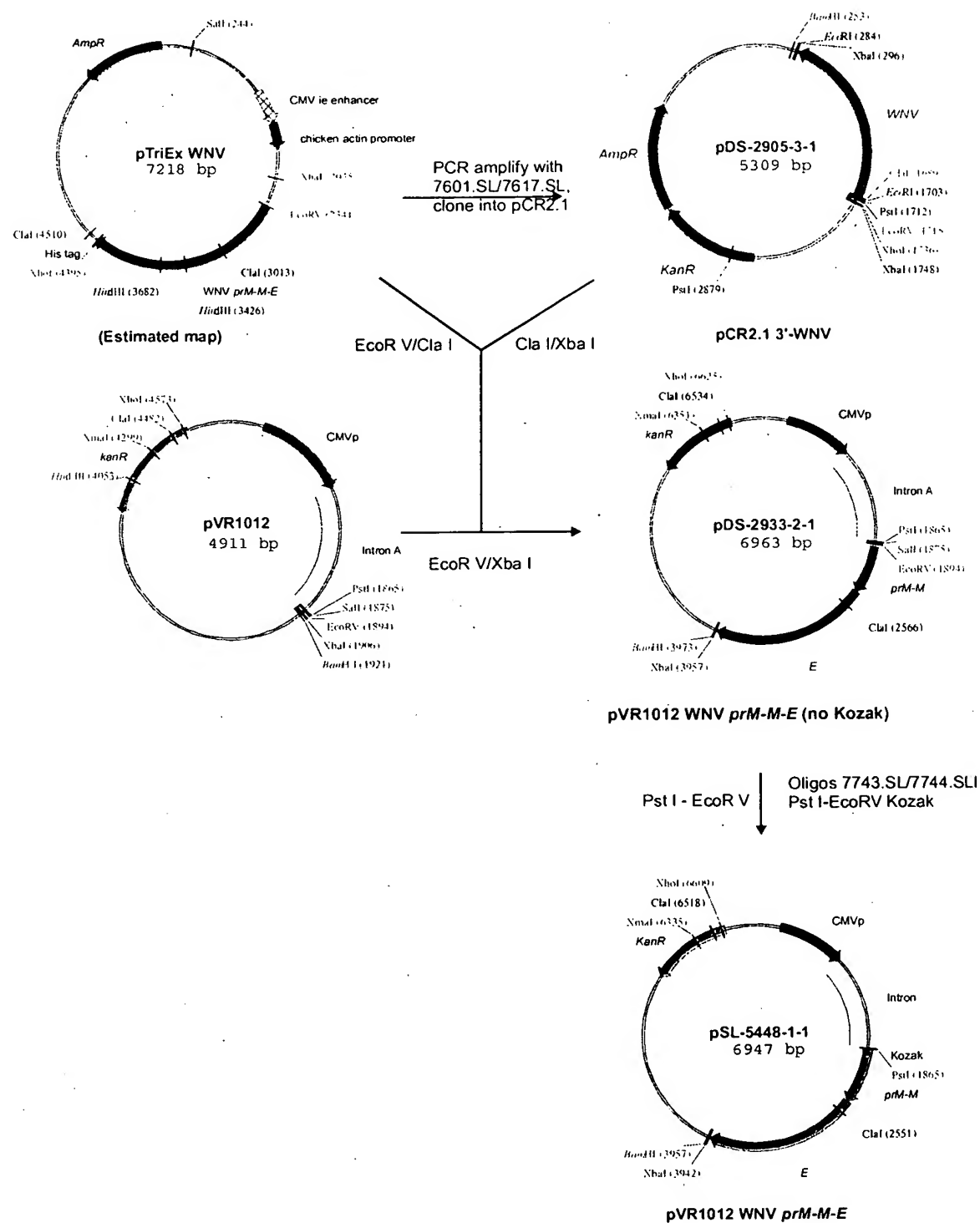


Figure 8. Nucleotide sequence and translation of the WNV *prM-M-E* region in pSL-5448-1-1, pVR1012 WNV *prM-M-E*.

```

PstI      Kozak      ⇒ WNV capsid leader
          M G S T G I A V M I G L I A S V .
1  CTGCAGCCGC CACCATGGGA TCAACCGGAA TTGCAGTCAT GATTGGCCTG ATCGCCAGCG

          ⇒ WNV prM
          .. G A V T L S N F Q G K V M M T V N A T D .
61  TAGGAGCAGT TACCCTCTCT AACTTCCAAG GGAAGGTGAT GATGACGGTA AATGCTACTG

          .. V T D V I T I P T A A G K N L C I V R A .
121 ACGTACAGA TGTCATCAG ATTCCAACAG CTGCTGGAAA GAACCTATGC ATTGTCAGAG

          .. M D V G Y M C D D T I T Y E C P V L S A .
181 CAATGGATGT GGGATACATG TCGATGATA CTATCACTTA TGAATGCCCA GTGCTGTGCG

          .. G N D P E D I D C W C T K S A V Y V R Y .
241 CTGGTAATGA TCCAGAAGAC ATCGACTGTT GGTGCACAAA GTCAGCAGTC TACGTCAGGT

          ⇒ WNV M
          .. G R C T K T R H S R R S R R S L T V Q T .
301 ATGGAAGATG CACCAAGACA CGCCACTCAA GACGCAGTCG GAGGTCCTG ACAGTGCAGA

          .. H G E S T L A N K K G A W M D S T K A T .
361 CACACGGAGA AAGCACTCTA GCGAACAAGA AGGGGGCTTG GATGGACAGC ACCAAGGCCA

          .. R Y L V K T E S W I L R N P G Y A L V A .
421 CAAGGTATTT GGTA AAAACA GAATCATGGA TCTTGAGGAA CCCTGGATAT GCCCTGGTGG

          .. A V I G W M L G S N T M Q R V V F V V L .
481 CAGCCGTCAT TGGTTGGATG CTTGGGAGCA ACACCATGCA GAGAGTTGTG TTTGTCTGTC

          ⇒ WNV E
          .. L L L V A P A Y S F N C L G M S N R D F .
541 TATTGCTTTT GTTGCCCCA GCTTACAGCT TCAACTGCCT TGGAATGAGC AACAGAGACT

          .. L E G V S G A T W V D L V L E G D S C V .
601 TCTTGAAGG AGTGTCTGGA GCAACATGGG TGGATTGGT TCTCGAAGGC GACAGCTGCG

          ClaI
          .. T I M S K D K P T I D V K M M N M E A A .
661 TGACTATCAT GTCTAAGGAC AAGCCTACCA TCGATGTGAA GATGATGAAT ATGGAGGCGG

          .. N L A E V R S Y C Y L A T V S D L S T K .
721 CCAACCTGGC AGAGGTCCGC AGTTATTGCT ATTTGGCTAC CGTCAGCGAT CTCTCCACCA

          .. A A C P T M G E A H N D K R A D P A F V .
781 AAGCTGCGTG CCCGACCATG GGAGAAGCTC ACAATGACAA ACGTGCTGAC CCAGCTTTTTG

          .. C R Q G V V D R G W G N G C G L F G K G .
841 TGTGCAGACA AGGAGTGGTG GACAGGGGCT GGGGCAACGG CTGCGGACTA TTTGGCAAAG

          .. S I D T C A K F A C S T K A I G R T I L .
901 GAAGCATTGA CACATGCGCC AAATTTGCCT GCTCTACCAA GGCAATAGGA AGAACCATCT

          .. K E N I K Y E V A I F V H G P T T V E S .
961 TGAAAGAGAA TATCAAGTAC GAAGTGGCCA TTTTGTCCA TGGACCAACT ACTGTGGAGT

          .. H G N Y S T Q V G A T Q A G R F S I T P .
1021 CGCACGGAAG CTACTCCACA CAGGTTGGAG CCACTCAGGC AGGGAGATTC AGCATCACTC

```

1081 .. A A P S Y T L K L G E Y G E V T V D C E .
 CTGCGGCGCC TTCATACACA CTAAAGCTTG GAGAATATGG AGAGGTGACA GTGGACTGTG
 1141 .. P R S G I D T N A Y Y V M T V G T K T F .
 AACACGGGTC AGGGATTGAC ACCAATGCAT ACTACGTGAT GACTGTTGGA ACAAAGACGT
 1201 .. L V H R E W F M D L N L P W S S A G S T .
 TCTTGGTCCA TCGTGAGTGG TTCATGGACC TCAACCTCCC TTGGAGCAGT GCTGGAAGTA
 1261 .. V W R N R E T L M E F E E P H A T K Q S .
 CTGTGTGGAG GAACAGAGAG ACGTTAATGG AGTTTGAGGA ACCACACGCC ACCAAGCAGT
 1321 .. V I A L G S Q E G A L H Q A L A G A I P .
 CTGTGATAGC ATTGGGCTCA CAAGAGGGAG CTCTGCATCA AGCTTTGGCT GGAGCCATTC
 1381 .. V E F S S N T V K L T S G H L K C R V K .
 CTGTGGAATT TTCAAGCAAC ACTGTCAAGT TGACGTCGGG TCATTTGAAG TGTAGAGTGA
 1441 .. M E K L Q L K G T T Y G V C S K A F K F .
 AGATGGAAAA ATTGCAGTTG AAGGGAACAA CCTATGGCGT CTGTTCAAAG GCTTTCAAGT
 1501 .. L G T P A D T G H G T V V L E L Q Y T G .
 TTCTTGGGAC TCCCGCAGAC ACAGGTCACG GCACTGTGGT GTTGAATTG CAGTACACTG
 1561 .. T D G P C K V P I S S A A S L N D L T P .
 GCACGGATGG ACCTTGCAAA GTTCCTATCT CGTCAGCGGC TTCATTGAAC GACCTAACGC
 1621 .. V G R L V T V N P F V S V A T A N A K V .
 CAGTGGGCAG ATTGGTCACT GTCAACCCCTT TTGTTTCAGT GGCCACGGCC AACGCTAAGG
 1681 .. L I E L E P P F G D S Y I V V G R G E Q .
 TCCTGATTGA ATTGGAACCA CCCTTTGGAG ACTCATACAT AGTGGTGGGC AGAGGAGAAC
 1741 .. Q I N H H W H K S G S S I G K A F T T T .
 AACAGATCAA TCACCATTGG CACAAGTCTG GAAGCAGCAT TGGCAAAGCC TTTACAACCA
 1801 .. L K G A Q R L A A L G D T A W D F G S V .
 CCCTCAAAGG AGCGCAGAGA CTAGCCGCTC TAGGAGACAC AGCTTGGGAC TTTGGATCAG
 1861 .. G G V F T S V G K A V H Q V F G G A F R .
 TTGGAGGGGT GTTCACCTCA GTTGGGAAGG CTGTCCATCA AGTGTTCCGA GGAGCATTCC
 1921 .. S L F G G M S W I T Q G L L G A L L L W .
 GCTCACTGTT CGGAGGCATG TCCTGGATAA CGCAAGGATT GCTGGGGGCT CTCCTGTTGT
 1981 .. M G I N A R D R S I A L T F L A V G G V .
 GGATGGGCAT CAATGCTCGT GATAGGTCCA TAGCTCTCAC GTTCTCGCA GTTGGAGGAG
 2041 .. L L F L S V N V H A
 TTCTGCTCTT CCTCTCCGTG AACGTGCACG CTTAATTTTT ATCTAGA

XbaI

ATCTAGA

FIGURE 9Sequence of pDS-2946-1-1, pC5 H6p WNV *prM-M-E*.

1 GCGCCCAATACGCAAACCGCCTCTCCCCGCGGTTGGCCGATTCAATTAATGCAGCTGGCA
61 CGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCT
121' CACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAAT
181 TGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGAATTGCGGCC \Rightarrow C5R
241 GCAATTCTGAATGTTAAATGTTATACTTTGGATGAAGCTATAAATATGCATTGGAAAAAT
301 AATCCATTTAAAGAAAGGATTCAAATACTACAAAACCTAAGCGATAATATGTTAACTAAG
361 CTTATTCTTAACGACGCTTTAAATATACACAAATAAACATAATTTTGTATAACCTAACA
421 AATAACTAAAACATAAAAAATAATAAAGGAAATGTAATATCGTAATTATTTTACTCAGGA
481 ATGGGGTTAAATATTTATATCACGTGTATATCTATACTGTTATCGTATACTCTTTACAAT
541 TACTATTACGAATATGCAAGAGATAATAAGATTACGTATTTAAGAGAATCTTGTCATGAT
601 AATTGGGTACGACATAGTGATAAATGCTATTTTCGCATCGTTACATAAAGTCAGTTGGAAA
661 GATGGATTTGACAGATGTAACCTTAATAGGTGCAAAAATGTTAAATAACAGCATTCTATCG
721 GAAGATAGGATACCAGTTATATTATACAAAATCACTGGTTGGATAAAACAGATTCTGCA
781 ATATTCGTAAAAGATGAAGATTACTGCGAATTTGTAACTATGACAATAAAAAGCCATTT
841 ATCTCAACGACATCGTGTAATTCCTTCATGTTTTATGTATGTGTTTCAGATATTATGAGA
901 TTACTATAAACTTTTTGTATACTTATATTCCGTAACTATATTAATCATGAAGAAAATGA
961 AAAAGTATAGAAGCTGTTACAGAGCGGTTGTTGAAAACAACAAAATTATACATTCAAGAT
1021 GGCTTACATATACGTCTGTGAGGCTATCATGGATAATGACAATGCATCTCTAAATAGGTT
1081 TTTGGACAATGGATTGACCCCTAACACGGAATATGGTACTCTACAATCTCCTCTTGAAAT
1141 GGCTGTAATGTTCAAGAATACCGAGGCTATAAAAATCTTGATGAGGTATGGAGCTAAACC
1201 TGTAGTTACTGAATGCACAACCTTCTGTCTGCATGATGCGGTGTTGAGAGACGACTACAA
1261 AATAGTGAAAGATCTGTTGAAGAATAACTATGTAAACAATGTTCTTTACAGCGGAGGCTT
1321 TACTCCTTTGTGTTTGGCAGCTTACCTTAACAAAGTTAATTTGGTTAACTTCTATTGGC
1381 TCATTCGGCGGATGTAGATATTTCAAACACGGATCGGTAACTCCTCTACATATAGCCGT
1441 ATCAAATAAAAATTTAACAATGGTTAACTTCTATTGAACAAAGGTGCTGATACTGACTT
1501 GCTGGATAACATGGGATGTACTCCTTTAATGATCGCTGTACAATCTGGAAATATTGAAAT

1561 ATGTAGCACACTACTTAAAAAAATAAAATGTCCAGAACTGGGAAAAATTGATCTTGCCA
1621 GCTGTAATTCATGGTAGAAAAGAAGTGCTCAGGCTACTTTTCAACAAAGGAGCAGATGTA
1681 AACTACATCTTTGAAAGAAATGGAAAATCATATACTGTTTTGGAATTGATTAAAGAAAGT
1741 TACTCTGAGACACAAAAGAGGTAGCTGAAGTGGTACTCTCAAAGGTACGTGACTAATTAG
1801 CTATAAAAAGGATCCGGGTTAATTAATTAGTCATCAGGCAGGGCGAGAACGAGACTATCT

⇒ H6p

1861 GCTCGTTAATTAATTAGAGCTTTCTTTATTCTATACTTAAAAAGTGAAAATAAATACAAAG
1921 GTTCTTGAGGGTTGTGTTAAATTGAAAGCGAGAAATAATCATAAATTATTTTCATTATCGC

⇒ WNV capsid leader

M T G I A V M I G L I A

1981 GATATCCGTTAAGTTTGTATCGTAATGACCGGAATTGCAGTCATGATTGGCCTGATCGCC

⇒ WNV prM start

2041 S V G A V T L S N F Q G K V M M T V N A
AGCGTAGGAGCGGTTACCCTCTCTAACTTCCAAGGAAGGTGATGATGACGGTAAATGCT

2101 T D V T D V I T I P T A A G K N L C I V
ACTGACGTCACAGATGTCATCAGATTCCAACAGCTGCTGGAAAGAACCTATGCATTGTC

2161 R A M D V G Y M C D D T I T Y E C P V L
AGAGCAATGGATGTGGGATACATGTGCGATGATACTATCACTTATGAATGCCAGTGCTG

2221 S A G N D P E D I D C W C T K S A V Y V
TCGGCTGGTAATGATCCAGAAGACATCGACTGTTGGTGCACAAAGTCAGCAGTCTACGTC

⇒ WNV M start

2281 R Y G R C T K T R H S R R S R R S L T V
AGGTATGGAAGATGCACCAAGACACGCCACTCAAGACGCAGTCGGAGGTCACTGACAGTG

Q T H G E S T L A N K K G A W M D S T K

2341 CAGACACACGGAGAAAGCACTCTAGCGAACAAGAAGGGGGCTTGGATGGACAGCACCAAG

2401 A T R Y L V K T E S W I L R N P G Y A L
GCCACAAGGTATTTGGTAAAAACAGAATCATGGATCTTGAGGAACCCTGGATATGCCCTG

2461 V A A V I G W M L G S N T M Q R V V F V
GTGGCAGCCGTCATTGGTTGGATGCTTGGGAGCAACACCATGCAGAGAGTTGTGTTTGTC

⇒ WNV E start

2521 V L L L L V A P A Y S F N C L G M S N R
GTGCTATTGCTTTTGGTGGCCCCAGCTTACAGCTTCAACTGCCTTGAATGAGCAACAGA

2581 D F L E G V S G A T W V D L V L E G D S
GACTTCTTGAAGGAGTGTCTGGAGCAACATGGGTGGATTTGGTTCTCGAAGGCGACAGC

2641 C V T I M S K D K P T I D V K M M N M E
TGCGTGACTATCATGTCTAAGGACAAGCCTACCATCGATGTGAAGATGATGAATATGGAG

2701 A A N L A E V R S Y C Y L A T V S D L S
 GCGGCCAACCTGGCAGAGGTCCGCAGTTATTGCTATTTGGCTACCGTCAGCGATCTCTCC

2761 T K A A C P T M G E A H N D K R A D P A
 ACCAAAGCTGCGTGCCCCGACCATGGGAGAAGCTCACAATGACAAACGTGCTGACCCAGCT

2821 F V C R Q G V V D R G W G N G C G L F G
 TTTGTGTGCAGACAAGGAGTGGTGGACAGGGGCTGGGGCAACGGCTGCGGACTATTTGGC

2881 K G S I D T C A K F A C S T K A I G R T
 AAAGGAAGCATTGACACATGCGCCAAATTTGCCTGCTCTACCAAGGCAATAGGAAGAACC

2941 I L K E N I K Y E V A I F V H G P T T V
 ATCTTGAAAGAGAATATCAAGTACGAAGTGGCCATCTTCGTGCACGGACCAACTACTGTG

3001 E S H G N Y S T Q V G A T Q A G R F S I
 GAGTCGCACGGAAACTACTCCACACAGGTTGGAGCCACTCAGGCAGGGAGATTTCAGCATC

3061 T P A A P S Y T L K L G E Y G E V T V D
 ACTCCTGCGGCGCCTTCATACACACTAAAGCTTGGAGAATATGGAGAGGTGACAGTGGAC

3121 C E P R S G I D T N A Y Y V M T V G T K
 TGTGAACCACGGTCAGGGATTGACACCAATGCATACTACGTGATGACTGTTGGAACAAAG

3181 T F L V H R E W F M D L N L P W S S A G
 ACGTTCTTGGTCCATCGTGAGTGGTTCATGGACCTCAAQCTCCCTTGGAGCAGTGCTGGA

3241 S T V W R N R E T L M E F E E P H A T K
 AGTACTGTGTGGAGGAACAGAGAGACGTTAATGGAGTTTGAGGAACCACACGCCACGAAG

3301 Q S V I A L G S Q E G A L H Q A L A G A
 CAGTCTGTGATAGCATTGGGCTCACAAGAGGGAGCTCTGCATCAAGCTTTGGCTGGAGCC

3361 I P V E F S S N T V K L T S G H L K C R
 ATTCCTGTGGAATTTTCAAGCAACACTGTCAAGTTGACGTGCGGTCATTGAAAGTGTAGA

3421 V K M E K L Q L K G T T Y G V C S K A F
 GTGAAGATGGAAAAATTGCAGTTGAAGGGAACAACCTATGGCGTCTGTTCAAAGGCTTTC

3481 K F L G T P A D T G H G T V V L E L Q Y
 AAGTTTCTTGGGACTCCCGCAGACACAGGTACGGCACTGTGGTGTGGAATTGCAGTAC

3541 T G T D G P C K V P I S S A A S L N D L
 ACTGGCACGGATGGACCTTGCAAAGTTCCTATCTCGTCAGCGGCTTCATTGAACGACCTA

3601 T P V G R L V T V N P F V S V A T A N A
 ACGCCAGTGGGCAGATTGGTCACTGTCAACCCTTTTGTTCAGTGGCCACGGCCAACGCT

3661 K V L I E L E P P F G D S Y I V V G R G
 AAGGTCCTGATTGAATTGGAACCACTTTGGAGACTCATACATAGTGGTGGGCAGAGGA

3721 E Q Q I N H H W H K S G S S I G K A F T
 GAACAACAGATCAATCACCATTGGCACAAGTCTGGAAGCAGCATTGGCAAAGCCTTTACA

3781 T T L K G A Q R L A A L G D T A W D F G
ACCACCCTCAAAGGAGCGCAGAGACTAGCCGCTCTAGGAGACACAGCTTGGGACTTTGGA
3841 S V G G V F T S V G K A V H Q V F G G A
TCAGTTGGAGGGGTGTTACCTCAGTTGGGAAGGCTGTCCATCAAGTGTTCGGAGGAGCA
3901 F R S L F G G M S W I T Q G L L G A L L
TTCCGCTCACTGTTTCGGAGGCATGTCTGGATAACGCAAGGATTGCTGGGGGCTCTCCTG
3961 L W M G I N A R D R S I A L T F L A V G
TTGTGGATGGGCATCAATGCTCGTGATAGGTCCATAGCTCTCACGTTTCTCGCAGTTGGA

⇒ C5L

4021 G V L L F L S V N V H A *
GGAGTTCTGCTCTTCCTCTCCGTGAACGTGCACGCTTAATTTTTATCTAGAATCGATCCC
4081 GGGTTTTTATGACTAGTTAATCACGGCCGCTTATAAAGATCTAAAATGCATAATTTCTAA
4141 ATAATGAAAAAAGTACATCATGAGCAACGCGTTAGTATATTTTACAATGGAGATTAAACG
4201 CTCTATACCGTTCTATGTTTATTGATTGAGATGATGTTTTAGAAAAGAAAGTTATTGAAT
4261 ATGAAAACCTTTAATGAAGATGAAGATGACGACGATGATTATTGTTGTAAATCTGTTTTAG
4321 ATGAAGAAGATGACGCGCTAAAGTATACTATGGTTACAAAGTATAAGTCTATACTACTAA
4381 TGGCGACTTGTGCAAGAAGGTATAGTATAGTGAAAATGTTGTTAGATTATGATTATGAAA
4441 AACCATAAATCAGATCCATATCTAAAGGTATCTCCTTTGCACATAATTTTCATCTATTC
4501 CTAGTTTAGAATACCTGCAGCCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACT
4561 GGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCT
4621 GGCCTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATG
4681 GCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCA
4741 TATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACC
4801 CGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGAC
4861 AAGCTGTGACCGTCTCCGGGAGCTGCATGTGTGAGAGGTTTTACCGTCATCACCGAAAC
4921 GCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAA
4981 TGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTT
5041 TATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGC
5101 TTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTGCGCCCTTATTC
5161 CCTTTTTTGCGGCATTTTGCCCTTCTGTTTTTGCTCACCAGAAACGCTGGTGAAAGTAA
5221 AAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCG
5281 GTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAG

5341 TTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTGCGC
5401 GCATACACTATTCTCAGAATGACTTGTTGAGTACTCACCAGTCACAGAAAAGCATCTTA
5461 CGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAAACTG
5521 CGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACA
5581 ACATGGGGGATCATGTAACCTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATAC
5641 CAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAATAT
5701 TAACTGGCGAACTACTTACTCTAGCTTCCCGCAACAATTAATAGACTGGATGGAGGCGG
5761 ATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATA
5821 AATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTA
5881 AGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAA
5941 ATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAG
6001 TTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAGGATCTAGG
6061 TGAAGATCCTTTTTGATAATCTCATGACCAAATCCCTTAACGTGAGTTTTCTGTTCCACT
6121 GAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCG
6181 TAATCTGCTGCTTGCAAACAAAAAACCACCGCTACCAGCGGTGGTTTGTGTTGCCGGATC
6241 AAGAGCTACCAACTCTTTTTCCGAAGGTAACCTGGCTTCAGCAGAGCGCAGATACCAAATA
6301 CTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTA
6361 CATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCTGTGTC
6421 TTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGG
6481 GGGGTTCTGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTAC
6541 AGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGG
6601 TAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGAAACGCCTGGT
6661 ATCTTTATAGTCTGTGCGGTTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCT
6721 CGTCAGGGGGGCGGAGCCTATGGAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGG
6781 CCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATA
6841 ACCGTATTACGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCA
6901 GCGAGTCAGTGAGCGAGGAAGCGGAAGA

FIGURE 10

Construction of pC5 H6p WNV *prM-M-E* donor plasmids with a truncated H6p +/- truncated WNV capsid leader sequence.

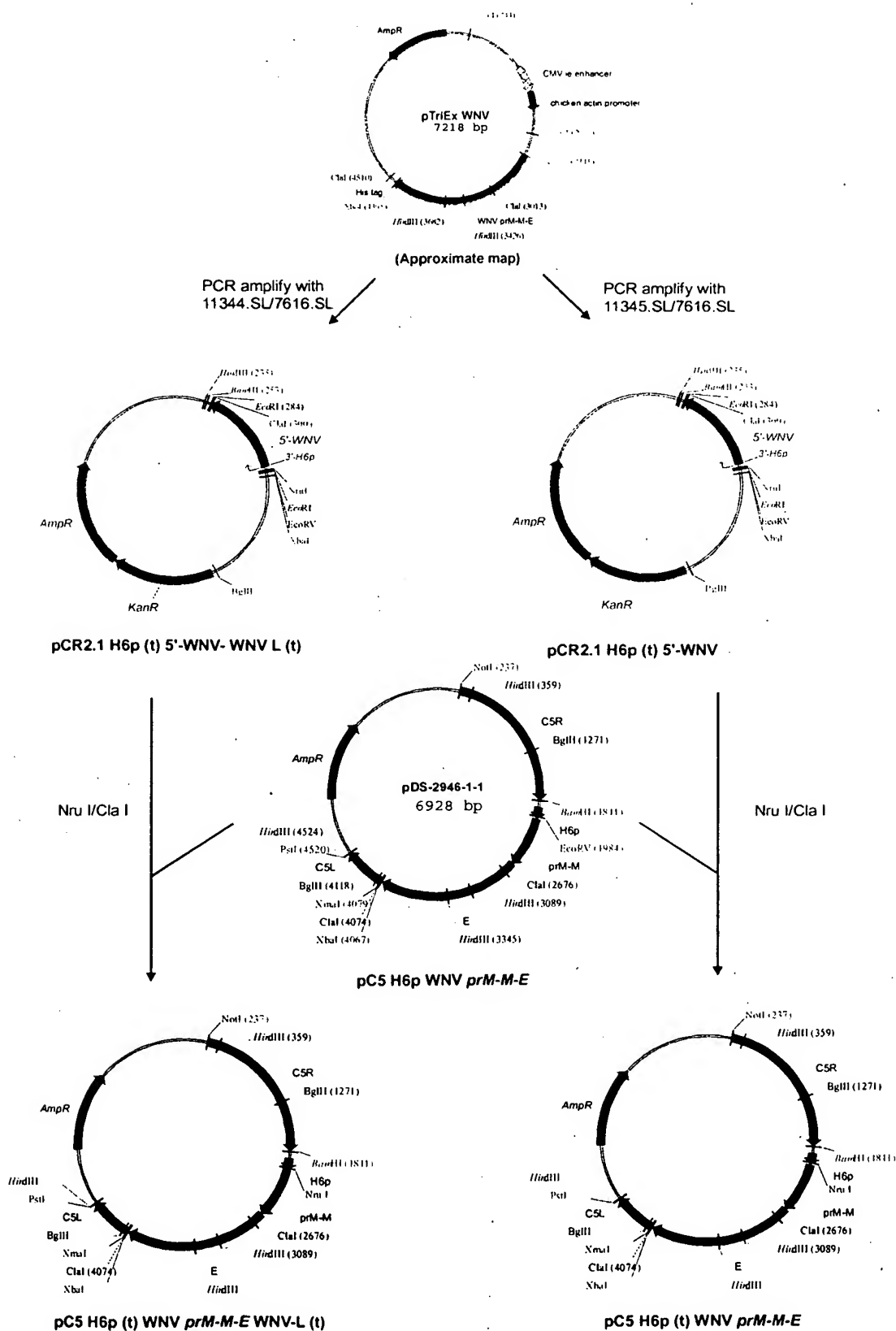


FIGURE 11

ALVAC WNV constructs with truncated H6p +/- truncated leader sequence

Explanation of terms:

H6p (t) is the truncated H6p promoter deleted between Nru I and the 3'-end

WNV-L (t) refers to the truncated WNV capsid leader, which is missing the initiating Met, so results in a shorter leader sequence

H6p 5'-WNV sequence in actual vCP2017:

```

                                     ⇒ H6p
1861  GCTCGTTAATTAATTAGAGCTTCTTTATTCTATACTTAAAAAGTGAAAATAAATACAAAG
                                     Nru I
1921  GTTCTTGAGGGTTGTGTTAAATTGAAAGCGAGAAATAATCATAAATTATTCATTATCGC
                                     ⇒ WNV capsid leader
                                     M T G I A V M I G L I A
1981  GATTATCCGTTAAGTTTGTATCGTAATGACCGGAATTGCAGTCATGATTGGCCTGATCGCC
                                     ⇒ WNV prM start
                                     S V G A V T L S N F Q G K V M M T V N A
2041  AGCGTAGGAGCGGTTACCCTCTCTAACTTCCAAGGAAGGTGATGATGACGGTAAATGCT
                                     T D V T D V I T I P T A A G K N L C I V
2101  ACTGACGTCACAGATGTCATCACGATTCCAACAGCTGCTGGAAAGAACCTATGCATTGTC
```

PCR primers for H6p (t) WNV *prM-M-E* WNV-L (t):

```

                                     ⇒ WNV capsid
                                     NruI  T G I A V M I G L
11344.SL  5'  ATTATCGCGAACCGGAATTGCAGTCATGATTGGCCTG
                                     K P T I D V K M
                                     AAGCCTACCATCGATGTGAAGATG
7616.SL   3'  TTCGGATGGTAGCTACACTTCTAC
                                     Cla I
```

PCR primers for H6p (t) WNV *prM-M-E*:

```

                                     ⇒ WNV capsid
                                     NruI  M T G I A V M I G L
11345.SL  5'  ATTATCGCGAATGACCGGAATTGCAGTCATGATTGGCCTG
```

FIGURE 12

agtagttcgc ctgtgtgagc tgacaaactt agtagtgttt gtgaggatta acaacaatta
60

acacagtgcg agctgtttct tagcacgaag atctcg atg tct aag aaa cca gga
114

Met Ser Lys Lys Pro Gly
1 5

ggg ccc ggc aag agc cgg gct gtc aat atg cta aaa cgc gga atg ccc
162

Gly Pro Gly Lys Ser Arg Ala Val Asn Met Leu Lys Arg Gly Met Pro
10 15 20

cgc gtg ttg tcc ttg att gga ctg aag agg gct atg ttg agc ctg atc
210

Arg Val Leu Ser Leu Ile Gly Leu Lys Arg Ala Met Leu Ser Leu Ile
25 30 35

gac ggc aag ggg cca ata cga ttt gtg ttg gct ctc ttg gcg ttc ttc
258

Asp Gly Lys Gly Pro Ile Arg Phe Val Leu Ala Leu Leu Ala Phe Phe
40 45 50

agg ttc aca gca att gct ccg acc cga gca gtg ctg gat cga tgg aga
306

Arg Phe Thr Ala Ile Ala Pro Thr Arg Ala Val Leu Asp Arg Trp Arg
55 60 65 70

ggt gtg aac aaa caa aca gcg atg aaa cac ctt ctg agt ttt aag aag
354

Gly Val Asn Lys Gln Thr Ala Met Lys His Leu Leu Ser Phe Lys Lys
75 80 85

gaa cta ggg acc ttg acc agt gct atc aat cgg cgg agc tca aaa caa
402

Glu Leu Gly Thr Leu Thr Ser Ala Ile Asn Arg Arg Ser Ser Lys Gln
90 95 100

aag aaa aga gga gga aag acc gga att gca gtc atg att ggc ctg atc
450

Lys Lys Arg Gly Gly Lys Thr Gly Ile Ala Val Met Ile Gly Leu Ile
105 110 115

gcc agc gta gga gca gtt acc ctc tct aac ttc caa ggg aag gtg atg
498

Ala Ser Val Gly Ala Val Thr Leu Ser Asn Phe Gln Gly Lys Val Met
120 125 130

atg acg gta aat gct act gac gtc aca gat gtc atc acg att cca aca
546

Met Thr Val Asn Ala Thr Asp Val Thr Asp Val Ile Thr Ile Pro Thr
135 140 145 150

gct gct gga aag aac cta tgc att gtc aga gca atg gat gtg gga tac
594

Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp Val Gly Tyr
155 160 165

atg tgc gat gat act atc act tat gaa tgc cca gtg ctg tcg gct ggt
642

Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu Ser Ala Gly
170 175 180

aat gat cca gaa gac atc gac tgt tgg tgc aca aag tca gca gtc tac
690

Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser Ala Val Tyr
185 190 195

gtc agg tat gga aga tgc acc aag aca cgc cac tca aga cgc agt cgg
738

Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg Arg Ser Arg
200 205 210

agg tca ctg aca gtg cag aca cac gga gaa agc act cta gcg aac aag
786

Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu Ala Asn Lys
215 220 225 230

aag ggg gct tgg atg gac agc acc aag gcc aca agg tat ttg gta aaa
834

Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr Leu Val Lys
235 240 245

aca gaa tca tgg atc ttg agg aac cct gga tat gcc ctg gtg gca gcc
882

Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu Val Ala Ala
250 255 260

gtc att ggt tgg atg ctt ggg agc aac acc atg cag aga gtt gtg ttt
930

Val Ile Gly Trp Met Leu Gly Ser Asn Thr Met Gln Arg Val Val Phe
265 270 275

gtc gtg cta ttg ctt ttg gtg gcc cca gct tac agc ttc aac tgc ctt
978

Val Val Leu Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu
280 285 290

gga atg agc aac aga gac ttc ttg gaa gga gtg tct gga gca aca tgg
1026

Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser Gly Ala Thr Trp
 295 300 305 310

gtg gat ttg gtt ctc gaa ggc gac agc tgc gtg act atc atg tct aag
 1074

Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile Met Ser Lys
 315 320 325

gac aag cct acc atc gat gtg aag atg atg aat atg gag gcg gcc aac
 1122

Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu Ala Ala Asn
 330 335 340

ctg gca gag gtc cgc agt tat tgc tat ttg gct acc gtc agc gat ctc
 1170

Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr Val Ser Asp Leu
 345 350 355

tcc acc aaa gct gcg tgc ccg acc atg gga gaa gct cac aat gac aaa
 1218

Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala His Asn Asp Lys
 360 365 370

cgt gct gac cca gct ttt gtg tgc aga caa gga gtg gtg gac agg ggc
 1266

Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val Val Asp Arg Gly
 375 380 385 390

tgg ggc aac ggc tgc gga cta ttt ggc aaa gga agc att gac aca tgc
 1314

Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys
 395 400 405

gcc aaa ttt gcc tgc tct acc aag gca ata gga aga acc atc ttg aaa
 1362

Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg Thr Ile Leu Lys
 410 415 420

gag aat atc aag tac gaa gtg gcc att ttt gtc cat gga cca act act
 1410

Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly Pro Thr Thr
 425 430 435

gtg gag tcg cac gga aac tac tcc aca cag gtt gga gcc act cag gca
 1458

Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly Ala Thr Gln Ala
 440 445 450

ggg aga ttc agc atc act cct gcg gcg cct tca tac aca cta aag ctt
 1506

Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr Thr Leu Lys Leu
 455 460 465 470

gga gaa tat gga gag gtg aca gtg gac tgt gaa cca cgg tca ggg att
1554

Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro Arg Ser Gly Ile
475 480 485

gac acc aat gca tac tac gtg atg act gtt gga aca aag acg ttc ttg
1602

Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr Lys Thr Phe Leu
490 495 500

gtc cat cgt gag tgg ttc atg gac ctc aac ctc cct tgg agc agt gct
1650

Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro Trp Ser Ser Ala
505 510 515

gga agt act gtg tgg agg aac aga gag acg tta atg gag ttt gag gaa
1698

Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met Glu Phe Glu Glu
520 525 530

cca cac gcc acg aag cag tct gtg ata gca ttg ggc tca caa gag gga
1746

Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly Ser Gln Glu Gly
535 540 545 550

gct ctg cat caa gct ttg gct gga gcc att cct gtg gaa ttt tca agc
1794

Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val Glu Phe Ser Ser
555 560 565

aac act gtc aag ttg acg tcg ggt cat ttg aag tgt aga gtg aag atg
1842

Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg Val Lys Met
570 575 580

gaa aaa ttg cag ttg aag gga aca acc tat ggc gtc tgt tca aag gct
1890

Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys Ser Lys Ala
585 590 595

ttc aag ttt ctt ggg act ccc gca gac aca ggt cac ggc act gtg gtg
1938

Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His Gly Thr Val Val
600 605 610

ttg gaa ttg cag tac act ggc acg gat gga cct tgc aaa gtt cct atc
1986

Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys Lys Val Pro Ile
615 620 625 630

tcg tca gtg gct tca ttg aac gac cta acg cca gtg ggc aga ttg gtc
2034

Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val Gly Arg Leu Val
635 640 645

act gtc aac cct ttt gtt tca gtg gcc acg gcc aac gct aag gtc ctg
2082

Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn Ala Lys Val Leu
650 655 660

att gaa ttg gaa cca ccc ttt gga gac tca tac ata gtg gtg ggc aga
2130

Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg
665 670 675

gga gaa caa cag atc aat cac cat tgg cac aag tct gga agc agc att
2178

Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser Gly Ser Ser Ile
680 685 690

ggc aaa gcc ttt aca acc acc ctc aaa gga gcg cag aga cta gcc gct
2226

Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala
695 700 705 710

cta gga gac aca gct tgg gac ttt gga tca gtt gga ggg gtg ttc acc
2274

Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Val Phe Thr
715 720 725

tca gtt ggg aag gct gtc cat caa gtg ttc gga gga gca ttc cgc tca
2322

Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Ser
730 735 740

ctg ttc gga ggc atg tcc tgg ata acg caa gga ttg ctg ggg gct ctc
2370

Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu Gly Ala Leu
745 750 755

ctg ttg tgg atg ggc atc aat gct cgt gat agg tcc ata gct ctc acg
2418

Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile Ala Leu Thr
760 765 770

ttt ctc gca gtt gga gga gtt ctg ctc ttc ctc tcc gtg aac gtg cac
2466

Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser Val Asn Val His
775 780 785 790

gct gac act ggg tgt gcc ata gac atc agc cgg caa gag ctg aga tgt
2514

Ala Asp Thr Gly Cys Ala Ile Asp Ile Ser Arg Gln Glu Leu Arg Cys
795 800 805

gga agt gga gtg ttc ata cac aat gat gtg gag gct tgg atg gac cgg
2562

Gly Ser Gly Val Phe Ile His Asn Asp Val Glu Ala Trp Met Asp Arg
810 815 820

tac aag tat tac cct gaa acg cca caa ggc cta gcc aag atc att cag
2610

Tyr Lys Tyr Tyr Pro Glu Thr Pro Gln Gly Leu Ala Lys Ile Ile Gln
825 830 835

aaa gct cat aag gaa gga gtg tgc ggt cta cga tca gtt tcc aga ctg
2658

Lys Ala His Lys Glu Gly Val Cys Gly Leu Arg Ser Val Ser Arg Leu
840 845 850

gag cat caa atg tgg gaa gca gtg aag gac gag ctg aac act ctt ttg
2706

Glu His Gln Met Trp Glu Ala Val Lys Asp Glu Leu Asn Thr Leu Leu
855 860 865 870

aag gag aat ggt gtg gac ctt agt gtc gtg gtt gag aaa cag gag gga
2754

Lys Glu Asn Gly Val Asp Leu Ser Val Val Val Glu Lys Gln Glu Gly
875 880 885

atg tac aag tca gca cct aaa cgc ctc acc gcc acc acg gaa aaa ttg
2802

Met Tyr Lys Ser Ala Pro Lys Arg Leu Thr Ala Thr Thr Glu Lys Leu
890 895 900

gaa att ggc tgg aag gcc tgg gga aag agt att tta ttt gca cca gaa
2850

Glu Ile Gly Trp Lys Ala Trp Gly Lys Ser Ile Leu Phe Ala Pro Glu
905 910 915

ctc gcc aac aac acc ttt gtg gtt gat ggt ccg gag acc aag gaa tgt
2898

Leu Ala Asn Asn Thr Phe Val Val Asp Gly Pro Glu Thr Lys Glu Cys
920 925 930

ccg act cag aat cgc gct tgg aat agc tta gaa gtg gag gat ttt gga
2946

Pro Thr Gln Asn Arg Ala Trp Asn Ser Leu Glu Val Glu Asp Phe Gly
935 940 945 950

ttt ggt ctc acc agc act cgg atg ttc ctg aag gtc aga gag agc aac
2994

Phe Gly Leu Thr Ser Thr Arg Met Phe Leu Lys Val Arg Glu Ser Asn
955 960 965

aca act gaa tgt gac tcg aag atc att gga acg gct gtc aag aac aac
3042

Thr Thr Glu Cys Asp Ser Lys Ile Ile Gly Thr Ala Val Lys Asn Asn
970 975 980

ttg gcg atc cac agt gac ctg tcc tat tgg att gaa agc agg ctc aat
3090

Leu Ala Ile His Ser Asp Leu Ser Tyr Trp Ile Glu Ser Arg Leu Asn
985 990 995

gat acg tgg aag ctt gaa agg gca gtt ctg ggt gaa gtc aaa tca
3135

Asp Thr Trp Lys Leu Glu Arg Ala Val Leu Gly Glu Val Lys Ser
1000 1005 1010

tgt acg tgg cct gag acg cat acc ttg tgg ggc gat gga atc ctt
3180

Cys Thr Trp Pro Glu Thr His Thr Leu Trp Gly Asp Gly Ile Leu
1015 1020 1025

gag agt gac ttg ata ata cca gtc aca ctg gcg gga cca cga agc
3225

Glu Ser Asp Leu Ile Ile Pro Val Thr Leu Ala Gly Pro Arg Ser
1030 1035 1040

aat cac aat cgg aga cct ggg tac aag aca caa aac cag ggc cca
3270

Asn His Asn Arg Arg Pro Gly Tyr Lys Thr Gln Asn Gln Gly Pro
1045 1050 1055

tgg gac gaa ggc cgg gta gag att gac ttc gat tac tgc cca gga
3315

Trp Asp Glu Gly Arg Val Glu Ile Asp Phe Asp Tyr Cys Pro Gly
1060 1065 1070

act acg gtc acc ctg agt gag agc tgc gga cac cgt gga cct gcc
3360

Thr Thr Val Thr Leu Ser Glu Ser Cys Gly His Arg Gly Pro Ala
1075 1080 1085

act cgc acc acc aca gag agc gga aag ttg ata aca gat tgg tgc
3405

Thr Arg Thr Thr Thr Glu Ser Gly Lys Leu Ile Thr Asp Trp Cys
1090 1095 1100

tgc agg agc tgc acc tta cca cca ctg cgc tac caa act gac agc
3450

Cys Arg Ser Cys Thr Leu Pro Pro Leu Arg Tyr Gln Thr Asp Ser
1105 1110 1115

ggc tgt tgg tat ggt atg gag atc aga cca cag aga cat gat gaa
3495

Gly Cys Trp Tyr Gly Met Glu Ile Arg Pro Gln Arg His Asp Glu
1120 1125 1130

aag acc ctc gtg cag tca caa gtg aat gct tat aat gct gat atg
3540

Lys Thr Leu Val Gln Ser Gln Val Asn Ala Tyr Asn Ala Asp Met
1135 1140 1145

att gac cct ttt cag ttg ggc ctt ctg gtc gtg ttc ttg gcc acc
3585

Ile Asp Pro Phe Gln Leu Gly Leu Leu Val Val Phe Leu Ala Thr
1150 1155 1160

cag gag gtc ctt cgc aag agg tgg aca gcc aag atc agc atg cca
3630

Gln Glu Val Leu Arg Lys Arg Trp Thr Ala Lys Ile Ser Met Pro
1165 1170 1175

gct ata ctg att gct ctg cta gtc ctg gtg ttt ggg ggc att act
3675

Ala Ile Leu Ile Ala Leu Leu Val Leu Val Phe Gly Gly Ile Thr
1180 1185 1190

tac act gat gtg tta cgc tat gtc atc ttg gtg ggg gca gct ttc
3720

Tyr Thr Asp Val Leu Arg Tyr Val Ile Leu Val Gly Ala Ala Phe
1195 1200 1205

gca gaa tct aat tcg gga gga gac gtg gta cac ttg gcg ctc atg
3765

Ala Glu Ser Asn Ser Gly Gly Asp Val Val His Leu Ala Leu Met
1210 1215 1220

gcg acc ttc aag ata caa cca gtg ttt atg gtg gca tcg ttt ctc
3810

Ala Thr Phe Lys Ile Gln Pro Val Phe Met Val Ala Ser Phe Leu
1225 1230 1235

aaa gcg aga tgg acc aac cag gag aac att ttg ttg atg ttg gcg
3855

Lys Ala Arg Trp Thr Asn Gln Glu Asn Ile Leu Leu Met Leu Ala
1240 1245 1250

gct gtt ttc ttt caa atg gct tat cac gat gcc cgc caa att ctg
3900

Ala Val Phe Phe Gln Met Ala Tyr His Asp Ala Arg Gln Ile Leu
1255 1260 1265

ctc tgg gag atc cct gat gtg ttg aat tca ctg gcg gta gct tgg
3945

Leu Trp 1270	Glu Ile Pro Asp Val 1275	Leu Asn Ser Leu Ala 1280	Val Ala Trp
atg ata 3990	ctg aga gcc ata aca	ttc aca acg aca tca	aac gtg gtt
Met Ile 1285	Leu Arg Ala Ile Thr 1290	Phe Thr Thr Thr Ser 1295	Asn Val Val
gtt ccg 4035	ctg cta gcc ctg cta	aca ccc ggg ctg aga	tgc ttg aat
Val Pro 1300	Leu Leu Ala Leu Leu 1305	Thr Pro Gly Leu Arg 1310	Cys Leu Asn
ctg gat 4080	gtg tac agg ata ctg	ctg ttg atg gtc gga	ata ggc agc
Leu Asp 1315	Val Tyr Arg Ile Leu 1320	Leu Leu Met Val Gly 1325	Ile Gly Ser
ttg atc 4125	agg gag aag agg agt	gca gct gca aaa aag	aaa gga gca
Leu Ile 1330	Arg Glu Lys Arg Ser 1335	Ala Ala Ala Lys Lys 1340	Lys Gly Ala
agt ctg 4170	cta tgc ttg gct cta	gcc tca aca gga ctt	ttc aac ccc
Ser Leu 1345	Leu Cys Leu Ala Leu 1350	Ala Ser Thr Gly Leu 1355	Phe Asn Pro
atg atc 4215	ctt gct gct gga ctg	att gca tgt gat ccc	aac cgt aaa
Met Ile 1360	Leu Ala Ala Gly Leu 1365	Ile Ala Cys Asp Pro 1370	Asn Arg Lys
cgc gga 4260	tgg ccc gca act gaa	gtg atg aca gct gtc	ggc cta atg
Arg Gly 1375	Trp Pro Ala Thr Glu 1380	Val Met Thr Ala Val 1385	Gly Leu Met
ttt gcc 4305	atc gtc gga ggg ctg	gca gag ctt gac att	gac tcc atg
Phe Ala 1390	Ile Val Gly Gly Leu 1395	Ala Glu Leu Asp Ile 1400	Asp Ser Met
gcc att 4350	cca atg act atc gcg	ggg ctc atg ttt gct	gct ttc gtg
Ala Ile 1405	Pro Met Thr Ile Ala 1410	Gly Leu Met Phe Ala 1415	Ala Phe Val
att tct 4395	ggg aaa tca aca gat	atg tgg att gag aga	acg gcg gac
Ile Ser 1420	Gly Lys Ser Thr Asp 1425	Met Trp Ile Glu Arg 1430	Thr Ala Asp

att tcc tgg gaa agt gat gca gaa att aca ggc tcg agc gaa aga
4440

Ile Ser Trp Glu Ser Asp Ala Glu Ile Thr Gly Ser Ser Glu Arg
1435 1440 1445

gtt gat gtg cgg ctt gat gat gat gga aac ttc cag ctc atg aat
4485

Val Asp Val Arg Leu Asp Asp Asp Gly Asn Phe Gln Leu Met Asn
1450 1455 1460

gat cca gga gca cct tgg aag ata tgg atg ctc aga atg gtc tgt
4530

Asp Pro Gly Ala Pro Trp Lys Ile Trp Met Leu Arg Met Val Cys
1465 1470 1475

ctc gcg att agt gcg tac acc ccc tgg gca atc ttg ccc tca gta
4575

Leu Ala Ile Ser Ala Tyr Thr Pro Trp Ala Ile Leu Pro Ser Val
1480 1485 1490

gtt gga ttt tgg ata act ctc caa tac aca aag aga gga ggc gtg
4620

Val Gly Phe Trp Ile Thr Leu Gln Tyr Thr Lys Arg Gly Gly Val
1495 1500 1505

ttg tgg gac act ccc tca cca aag gag tac aaa aag ggg gac acg
4665

Leu Trp Asp Thr Pro Ser Pro Lys Glu Tyr Lys Lys Gly Asp Thr
1510 1515 1520

acc acc ggc gtc tac agg atc atg act cgt ggg ctg ctc ggc agt
4710

Thr Thr Gly Val Tyr Arg Ile Met Thr Arg Gly Leu Leu Gly Ser
1525 1530 1535

tat caa gca gga gcg ggc gtg atg gtt gaa ggt gtt ttc cac acc
4755

Tyr Gln Ala Gly Ala Gly Val Met Val Glu Gly Val Phe His Thr
1540 1545 1550

ctt tgg cat aca aca aaa gga gcc gct ttg atg agc gga gag ggc
4800

Leu Trp His Thr Thr Lys Gly Ala Ala Leu Met Ser Gly Glu Gly
1555 1560 1565

cgc ctg gac cca tac tgg ggc agt gtc aag gag gat cga ctt tgt
4845

Arg Leu Asp Pro Tyr Trp Gly Ser Val Lys Glu Asp Arg Leu Cys
1570 1575 1580

tac gga gga ccc tgg aaa ttg cag cac aag tgg aac ggg cag gat
4890

Tyr Gly Gly Pro Trp Lys Leu Gln His Lys Trp Asn Gly Gln Asp
1585 1590 1595

gag gtg cag atg att gtg gtg gaa cct ggc aag aac gtt aag aac
4935

Glu Val Gln Met Ile Val Val Glu Pro Gly Lys Asn Val Lys Asn
1600 1605 1610

gtc cag acg aaa cca ggg gtg ttc aaa aca cct gaa gga gaa atc
4980

Val Gln Thr Lys Pro Gly Val Phe Lys Thr Pro Glu Gly Glu Ile
1615 1620 1625

ggg gcc gtg act ttg gac ttc ccc act gga aca tca ggc tca cca
5025

Gly Ala Val Thr Leu Asp Phe Pro Thr Gly Thr Ser Gly Ser Pro
1630 1635 1640

ata gtg gac aaa aac ggt gat gtg att ggg ctt tat ggc aat gga
5070

Ile Val Asp Lys Asn Gly Asp Val Ile Gly Leu Tyr Gly Asn Gly
1645 1650 1655

gtc ata atg ccc aac ggc tca tac ata agc gcg ata gtg cag ggt
5115

Val Ile Met Pro Asn Gly Ser Tyr Ile Ser Ala Ile Val Gln Gly
1660 1665 1670

gaa agg atg gat gag cca atc cca gcc gga ttc gaa cct gag atg
5160

Glu Arg Met Asp Glu Pro Ile Pro Ala Gly Phe Glu Pro Glu Met
1675 1680 1685

ctg agg aaa aaa cag atc act gta ctg gat ctc cat ccc ggc gcc
5205

Leu Arg Lys Lys Gln Ile Thr Val Leu Asp Leu His Pro Gly Ala
1690 1695 1700

ggt aaa aca agg agg att ctg cca cag atc atc aaa gag gcc ata
5250

Gly Lys Thr Arg Arg Ile Leu Pro Gln Ile Ile Lys Glu Ala Ile
1705 1710 1715

aac aga aga ctg aga aca gcc gtg cta gca cca acc agg gtt gtg
5295

Asn Arg Arg Leu Arg Thr Ala Val Leu Ala Pro Thr Arg Val Val
1720 1725 1730

gct gct gag atg gct gaa gca ctg aga gga ctg ccc atc cgg tac
5340

Ala 1735	Ala	Glu	Met	Ala	Glu	Ala 1740	Leu	Arg	Gly	Leu	Pro 1745	Ile	Arg	Tyr
cag 5385	aca	tcc	gca	gtg	ccc	aga	gaa	cat	aat	gga	aat	gag	att	gtt
Gln 1750	Thr	Ser	Ala	Val	Pro	Arg 1755	Glu	His	Asn	Gly	Asn 1760	Glu	Ile	Val
gat 5430	gtc	atg	tgt	cat	gct	acc	ctc	acc	cac	agg	ctg	atg	tct	cct
Asp 1765	Val	Met	Cys	His	Ala	Thr 1770	Leu	Thr	His	Arg	Leu 1775	Met	Ser	Pro
cac 5475	agg	gtg	ccg	aac	tac	aac	ctg	ttc	gtg	atg	gat	gag	gct	cat
His 1780	Arg	Val	Pro	Asn	Tyr	Asn 1785	Leu	Phe	Val	Met	Asp 1790	Glu	Ala	His
ttc 5520	acc	gac	cca	gct	agc	att	gca	gca	aga	ggc	tac	att	tcc	aca
Phe 1795	Thr	Asp	Pro	Ala	Ser	Ile 1800	Ala	Ala	Arg	Gly	Tyr 1805	Ile	Ser	Thr
aag 5565	gtc	gag	cta	ggg	gag	gcg	gcg	gca	ata	ttc	atg	aca	gcc	acc
Lys 1810	Val	Glu	Leu	Gly	Glu	Ala 1815	Ala	Ala	Ile	Phe	Met 1820	Thr	Ala	Thr
cca 5610	cca	ggc	act	tca	gat	cca	ttc	cca	gag	tcc	aat	tca	cca	att
Pro 1825	Pro	Gly	Thr	Ser	Asp	Pro 1830	Phe	Pro	Glu	Ser	Asn 1835	Ser	Pro	Ile
tcc 5655	gac	tta	cag	act	gag	atc	ccg	gat	cga	gct	tgg	aac	tct	gga
Ser 1840	Asp	Leu	Gln	Thr	Glu	Ile 1845	Pro	Asp	Arg	Ala	Trp 1850	Asn	Ser	Gly
tac 5700	gaa	tgg	atc	aca	gaa	tac	acc	ggg	aag	acg	gtt	tgg	ttt	gtg
Tyr 1855	Glu	Trp	Ile	Thr	Glu	Tyr 1860	Thr	Gly	Lys	Thr	Val 1865	Trp	Phe	Val
cct 5745	agt	gtc	aag	atg	ggg	aat	gag	att	gcc	ctt	tgc	cta	caa	cgt
Pro 1870	Ser	Val	Lys	Met	Gly	Asn 1875	Glu	Ile	Ala	Leu	Cys 1880	Leu	Gln	Arg
gct 5790	gga	aag	aaa	gta	gtc	caa	ttg	aac	aga	aag	tcg	tac	gag	acg
Ala 1885	Gly	Lys	Lys	Val	Val	Gln 1890	Leu	Asn	Arg	Lys	Ser 1895	Tyr	Glu	Thr

gag tac cca aaa tgt aag aac gat gat tgg gac ttt gtt atc aca
5835

Glu Tyr Pro Lys Cys Lys Asn Asp Asp Trp Asp Phe Val Ile Thr
1900 1905 1910

aca gac ata tct gaa atg ggg gct aac ttc aag gcg agc agg gtg
5880

Thr Asp Ile Ser Glu Met Gly Ala Asn Phe Lys Ala Ser Arg Val
1915 1920 1925

att gac agc cgg aag agt gtg aaa cca acc atc ata aca gaa gga
5925

Ile Asp Ser Arg Lys Ser Val Lys Pro Thr Ile Ile Thr Glu Gly
1930 1935 1940

gaa ggg aga gtg atc ctg gga gaa cca tct gca gtg aca gca gct
5970

Glu Gly Arg Val Ile Leu Gly Glu Pro Ser Ala Val Thr Ala Ala
1945 1950 1955

agt gcc gcc cag aga cgt gga cgt atc ggt aga aat ccg tcg caa
6015

Ser Ala Ala Gln Arg Arg Gly Arg Ile Gly Arg Asn Pro Ser Gln
1960 1965 1970

gtt ggt gat gag tac tgt tat ggg ggg cac acg aat gaa gac gac
6060

Val Gly Asp Glu Tyr Cys Tyr Gly Gly His Thr Asn Glu Asp Asp
1975 1980 1985

tcg aac ttc gcc cat tgg act gag gca cga atc atg ctg gac aac
6105

Ser Asn Phe Ala His Trp Thr Glu Ala Arg Ile Met Leu Asp Asn
1990 1995 2000

atc aac atg cca aac gga ctg atc gct caa ttc tac caa cca gag
6150

Ile Asn Met Pro Asn Gly Leu Ile Ala Gln Phe Tyr Gln Pro Glu
2005 2010 2015

cgt gag aag gta tat acc atg gat ggg gaa tac cgg ctc aga gga
6195

Arg Glu Lys Val Tyr Thr Met Asp Gly Glu Tyr Arg Leu Arg Gly
2020 2025 2030

gaa gag aga aaa aac ttt ctg gaa ctg ttg agg act gca gat ctg
6240

Glu Glu Arg Lys Asn Phe Leu Glu Leu Leu Arg Thr Ala Asp Leu
2035 2040 2045

cca gtt tgg ctg gct tac aag gtt gca gcg gct gga gtg tca tac
6285

Pro Val Trp Leu Ala Tyr Lys Val Ala Ala Ala Gly Val Ser Tyr
2050 2055 2060

cac gac cgg agg tgg tgc ttt gat ggt cct agg aca aac aca att
6330

His Asp Arg Arg Trp Cys Phe Asp Gly Pro Arg Thr Asn Thr Ile
2065 2070 2075

tta gaa gac aac aac gaa gtg gaa gtc atc acg aag ctt ggt gaa
6375

Leu Glu Asp Asn Asn Glu Val Glu Val Ile Thr Lys Leu Gly Glu
2080 2085 2090

agg aag att ctg agg ccg cgc tgg att gac gcc agg gtg tac tcg
6420

Arg Lys Ile Leu Arg Pro Arg Trp Ile Asp Ala Arg Val Tyr Ser
2095 2100 2105

gat cac cag gca cta aag gcg ttc aag gac ttc gcc tcg gga aaa
6465

Asp His Gln Ala Leu Lys Ala Phe Lys Asp Phe Ala Ser Gly Lys
2110 2115 2120

cgt tct cag ata ggg ctc att gag gtt ctg gga aag atg cct gag
6510

Arg Ser Gln Ile Gly Leu Ile Glu Val Leu Gly Lys Met Pro Glu
2125 2130 2135

cac ttc atg ggg aag aca tgg gaa gca ctt gac acc atg tac gtt
6555

His Phe Met Gly Lys Thr Trp Glu Ala Leu Asp Thr Met Tyr Val
2140 2145 2150

gtg gcc act gca gag aaa gga gga aga gct cac aga atg gcc ctg
6600

Val Ala Thr Ala Glu Lys Gly Gly Arg Ala His Arg Met Ala Leu
2155 2160 2165

gag gaa ctg cca gat gct ctt cag aca att gcc ttg att gcc tta
6645

Glu Glu Leu Pro Asp Ala Leu Gln Thr Ile Ala Leu Ile Ala Leu
2170 2175 2180

ttg agt gtg atg acc atg gga gta ttc ttc ctc ctc atg cag cgg
6690

Leu Ser Val Met Thr Met Gly Val Phe Phe Leu Leu Met Gln Arg
2185 2190 2195

aag ggc att gga aag ata ggt ttg gga ggc gct gtc ttg gga gtc
6735

Lys Gly	Ile Gly	Lys Ile	Gly Leu	Gly Gly	Ala Val	Leu Gly	Val
2200			2205			2210	
gcg acc	ttt ttc	tgt tgg	atg gct	gaa gtt	cca gga	acg aag	atc
6780							
Ala Thr	Phe Phe	Cys Trp	Met Ala	Glu Val	Pro Gly	Thr Lys	Ile
2215			2220			2225	
gcc gga	atg ttg	ctg ctc	tcc ctt	ctc ttg	atg att	gtg cta	att
6825							
Ala Gly	Met Leu	Leu Leu	Ser Leu	Leu Leu	Met Ile	Val Leu	Ile
2230			2235			2240	
cct gag	cca gag	aag caa	cgt tcg	cag aca	gac aac	cag cta	gcc
6870							
Pro Glu	Pro Glu	Lys Gln	Arg Ser	Gln Thr	Asp Asn	Gln Leu	Ala
2245			2250			2255	
gtg ttc	ctg att	tgt gtc	atg acc	ctt gtg	agc gca	gtg gca	gcc
6915							
Val Phe	Leu Ile	Cys Val	Met Thr	Leu Val	Ser Ala	Val Ala	Ala
2260			2265			2270	
aac gag	atg ggt	tgg cta	gat aag	acc aag	agt gac	ata agc	agt
6960							
Asn Glu	Met Gly	Trp Leu	Asp Lys	Thr Lys	Ser Asp	Ile Ser	Ser
2275			2280			2285	
ttg ttt	ggg caa	aga att	gag gtc	aag gag	aat ttc	agc atg	gga
7005							
Leu Phe	Gly Gln	Arg Ile	Glu Val	Lys Glu	Asn Phe	Ser Met	Gly
2290			2295			2300	
gag ttt	ctt ttg	gac ttg	agg ccg	gca aca	gcc tgg	tca ctg	tac
7050							
Glu Phe	Leu Leu	Asp Leu	Arg Pro	Ala Thr	Ala Trp	Ser Leu	Tyr
2305			2310			2315	
gct gtg	aca aca	gcg gtc	ctc act	cca ctg	cta aag	cat ttg	atc
7095							
Ala Val	Thr Thr	Ala Val	Leu Thr	Pro Leu	Leu Lys	His Leu	Ile
2320			2325			2330	
acg tca	gat tac	atc aac	acc tca	ttg acc	tca ata	aac gtt	cag
7140							
Thr Ser	Asp Tyr	Ile Asn	Thr Ser	Leu Thr	Ser Ile	Asn Val	Gln
2335			2340			2345	
gca agt	gca cta	ttc aca	ctc gcg	cga ggc	ttc ccc	ttc gtc	gat
7185							
Ala Ser	Ala Leu	Phe Thr	Leu Ala	Arg Gly	Phe Pro	Phe Val	Asp
2350			2355			2360	

gtt gga gtg tcg gct ctc ctg cta gca gcc gga tgc tgg gga caa
 7230
 Val Gly Val Ser Ala Leu Leu Leu Ala Ala Gly Cys Trp Gly Gln
 2365 2370 2375

gtc acc ctc acc gtt acg gta aca gcg gca aca ctc ctt ttt tgc
 7275
 Val Thr Leu Thr Val Thr Val Thr Ala Ala Thr Leu Leu Phe Cys
 2380 2385 2390

cac tat gcc tac atg gtt ccc ggt tgg caa gct gag gca atg cgc
 7320
 His Tyr Ala Tyr Met Val Pro Gly Trp Gln Ala Glu Ala Met Arg
 2395 2400 2405

tca gcc cag cgg cgg aca gcg gcc gga atc atg aag aac gct gta
 7365
 Ser Ala Gln Arg Arg Thr Ala Ala Gly Ile Met Lys Asn Ala Val
 2410 2415 2420

gtg gat ggc atc gtg gcc acg gac gtc cca gaa tta gag cgc acc
 7410
 Val Asp Gly Ile Val Ala Thr Asp Val Pro Glu Leu Glu Arg Thr
 2425 2430 2435

aca ccc atc atg cag aag aaa gtt gga cag atc atg ctg atc ttg
 7455
 Thr Pro Ile Met Gln Lys Lys Val Gly Gln Ile Met Leu Ile Leu
 2440 2445 2450

gtg tct cta gct gca gta gta gtg aac ccg tct gtg aag aca gta
 7500
 Val Ser Leu Ala Ala Val Val Val Asn Pro Ser Val Lys Thr Val
 2455 2460 2465

cga gaa gcc gga att ttg atc acg gcc gca gcg gtg acg ctt tgg
 7545
 Arg Glu Ala Gly Ile Leu Ile Thr Ala Ala Ala Val Thr Leu Trp
 2470 2475 2480

gag aat gga gca agc tct gtt tgg aac gca aca act gcc atc gga
 7590
 Glu Asn Gly Ala Ser Ser Val Trp Asn Ala Thr Thr Ala Ile Gly
 2485 2490 2495

ctc tgc cac atc atg cgt ggg ggt tgg ttg tca tgt cta tcc ata
 7635
 Leu Cys His Ile Met Arg Gly Gly Trp Leu Ser Cys Leu Ser Ile
 2500 2505 2510

Thr Trp Thr Leu Ile Lys Asn Met Glu Lys Pro Gly Leu Lys Arg
2515 2520 2525

Gly Gly Ala Lys Gly Arg Thr Leu Gly Glu Val Trp Lys Glu Arg
2530 2535 2540

Leu Asn Gln Met Thr Lys Glu Glu Phe Thr Arg Tyr Arg Lys Glu
2545 2550 2555

Ala Ile Ile Glu Val Asp Arg Ser Ala Ala Lys His Ala Arg Lys
2560 2565 2570

Glu Gly Asn Val Thr Gly Gly His Pro Val Ser Arg Gly Thr Ala
2575 2580 2585

Lys Leu Arg Trp Leu Val Glu Arg Arg Phe Leu Glu Pro Val Gly
2590 2595 2600

Lys Val Ile Asp Leu Gly Cys Gly Arg Gly Gly Trp Cys Tyr Tyr
2605 2610 2615

Met Ala Thr Gln Lys Arg Val Gln Glu Val Arg Gly Tyr Thr Lys
2620 2625 2630

Gly Gly Pro Gly His Glu Glu Pro Gln Leu Val Gln Ser Tyr Gly
2635 2640 2645

Trp Asn Ile Val Thr Met Lys Ser Gly Val Asp Val Phe Tyr Arg
2650 2655 2660

Pro	Ser	Glu	Cys	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser
2665						2670					2675			
tcg	tca	agt	gct	gag	gtt	gaa	gag	cat	agg	acg	att	cgg	gtc	ctt
8175														
Ser	Ser	Ser	Ala	Glu	Val	Glu	Glu	His	Arg	Thr	Ile	Arg	Val	Leu
2680						2685					2690			
gaa	atg	gtt	gag	gac	tgg	ctg	cac	cga	ggg	cca	agg	gaa	ttt	tgc
8220														
Glu	Met	Val	Glu	Asp	Trp	Leu	His	Arg	Gly	Pro	Arg	Glu	Phe	Cys
2695						2700					2705			
gtg	aag	gtg	ctc	tgc	ccc	tac	atg	ccg	aaa	gtc	ata	gag	aag	atg
8265														
Val	Lys	Val	Leu	Cys	Pro	Tyr	Met	Pro	Lys	Val	Ile	Glu	Lys	Met
2710						2715					2720			
gag	ctg	ctc	caa	cgc	cgg	tat	ggg	ggg	gga	ctg	gtc	aga	aac	cca
8310														
Glu	Leu	Leu	Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Asn	Pro
2725						2730					2735			
ctc	tca	cgg	aat	tcc	acg	cac	gag	atg	tat	tgg	gtg	agt	cga	gct
8355														
Leu	Ser	Arg	Asn	Ser	Thr	His	Glu	Met	Tyr	Trp	Val	Ser	Arg	Ala
2740						2745					2750			
tca	ggc	aat	gtg	gta	cat	tca	gtg	aat	atg	acc	agc	cag	gtg	ctc
8400														
Ser	Gly	Asn	Val	Val	His	Ser	Val	Asn	Met	Thr	Ser	Gln	Val	Leu
2755						2760					2765			
cta	gga	aga	atg	gaa	aaa	agg	acc	tgg	aag	gga	ccc	caa	tac	gag
8445														
Leu	Gly	Arg	Met	Glu	Lys	Arg	Thr	Trp	Lys	Gly	Pro	Gln	Tyr	Glu
2770						2775					2780			
gaa	gat	gta	aac	ttg	gga	agt	gga	acc	agg	gcg	gtg	gga	aaa	ccc
8490														
Glu	Asp	Val	Asn	Leu	Gly	Ser	Gly	Thr	Arg	Ala	Val	Gly	Lys	Pro
2785						2790					2795			
ctg	ctc	aac	tca	gac	acc	agt	aaa	atc	aag	aac	agg	att	gaa	cga
8535														
Leu	Leu	Asn	Ser	Asp	Thr	Ser	Lys	Ile	Lys	Asn	Arg	Ile	Glu	Arg
2800						2805					2810			
ctc	agg	cgt	gag	tac	agt	tcg	acg	tgg	cac	cac	gat	gag	aac	cac
8580														
Leu	Arg	Arg	Glu	Tyr	Ser	Ser	Thr	Trp	His	His	Asp	Glu	Asn	His
2815						2820					2825			

cca tat aga acc tgg aac tat cac ggc agt tat gat gtg aag ccc
 8625
 Pro Tyr Arg Thr Trp Asn Tyr His Gly Ser Tyr Asp Val Lys Pro
 2830 2835 2840

aca ggc tcc gcc agt tcg ctg gtc aat gga gtg gtc agg ctc ctc
 8670
 Thr Gly Ser Ala Ser Ser Leu Val Asn Gly Val Val Arg Leu Leu
 2845 2850 2855

tca aaa cca tgg gac acc atc acg aat gtt acc acc atg gcc atg
 8715
 Ser Lys Pro Trp Asp Thr Ile Thr Asn Val Thr Thr Met Ala Met
 2860 2865 2870

act gac act act ccc ttc ggg cag cag cga gtg ttc aaa gag aag
 8760
 Thr Asp Thr Thr Pro Phe Gly Gln Gln Arg Val Phe Lys Glu Lys
 2875 2880 2885

gtg gac acg aaa gct cct gaa ccg cca gaa gga gtg aag tac gtg
 8805
 Val Asp Thr Lys Ala Pro Glu Pro Pro Glu Gly Val Lys Tyr Val
 2890 2895 2900

ctc aat gag acc acc aac tgg ttg tgg gcg ttt ttg gcc aga gaa
 8850
 Leu Asn Glu Thr Thr Asn Trp Leu Trp Ala Phe Leu Ala Arg Glu
 2905 2910 2915

aaa cgt ccc aga atg tgc tct cga gag gaa ttc ata aga aag gtc
 8895
 Lys Arg Pro Arg Met Cys Ser Arg Glu Glu Phe Ile Arg Lys Val
 2920 2925 2930

aac agc aat gca gct ttg ggt gcc atg ttt gaa gag cag aat caa
 8940
 Asn Ser Asn Ala Ala Leu Gly Ala Met Phe Glu Glu Gln Asn Gln
 2935 2940 2945

tgg agg agc gcc aga gaa gca gtt gaa gat cca aaa ttt tgg gag
 8985
 Trp Arg Ser Ala Arg Glu Ala Val Glu Asp Pro Lys Phe Trp Glu
 2950 2955 2960

atg gtg gat gag gag cgc gag gca cat ctg cgg ggg gaa tgt cac
 9030
 Met Val Asp Glu Glu Arg Glu Ala His Leu Arg Gly Glu Cys His
 2965 2970 2975

act tgc att tac aac atg atg gga aag aga gag aaa aaa ccc gga
 9075
 Thr Cys Ile Tyr Asn Met Met Gly Lys Arg Glu Lys Lys Pro Gly
 2980 2985 2990

gag ttc gga aag gcc aag gga agc aga gcc att tgg ttc atg tgg
 9120
 Glu Phe Gly Lys Ala Lys Gly Ser Arg Ala Ile Trp Phe Met Trp
 2995 3000 3005

ctc gga gct cgc ttt ctg gag ttc gag gct ctg ggt ttt ctc aat
 9165
 Leu Gly Ala Arg Phe Leu Glu Phe Glu Ala Leu Gly Phe Leu Asn
 3010 3015 3020

gaa gac cac tgg ctt gga aga aag aac tca gga gga ggt gtc gag
 9210
 Glu Asp His Trp Leu Gly Arg Lys Asn Ser Gly Gly Gly Val Glu
 3025 3030 3035

ggc ttg ggc ctc caa aaa ctg ggt tac atc ctg cgt gaa gtt ggc
 9255
 Gly Leu Gly Leu Gln Lys Leu Gly Tyr Ile Leu Arg Glu Val Gly
 3040 3045 3050

acc cgg cct ggg ggc aag atc tat gct gat gac aca gct ggc tgg
 9300
 Thr Arg Pro Gly Gly Lys Ile Tyr Ala Asp Asp Thr Ala Gly Trp
 3055 3060 3065

gac acc cgc atc acg aga gct gac ttg gaa aat gaa gct aag gtg
 9345
 Asp Thr Arg Ile Thr Arg Ala Asp Leu Glu Asn Glu Ala Lys Val
 3070 3075 3080

ctt gag ctg ctt gat ggg gaa cat cgg cgt ctt gcc agg gcc atc
 9390
 Leu Glu Leu Leu Asp Gly Glu His Arg Arg Leu Ala Arg Ala Ile
 3085 3090 3095

att gag ctc acc tat cgt cac aaa gtt gtg aaa gtg atg cgc ccg
 9435
 Ile Glu Leu Thr Tyr Arg His Lys Val Val Lys Val Met Arg Pro
 3100 3105 3110

gct gct gat gga aga acc gtc atg gat gtt atc tcc aga gaa gat
 9480
 Ala Ala Asp Gly Arg Thr Val Met Asp Val Ile Ser Arg Glu Asp
 3115 3120 3125

cag agg ggg agt gga caa gtt gtc acc tac gcc cta aac act ttc
 9525

Gln Arg	Gly Ser Gly Gln Val	Val Thr Tyr Ala Leu	Asn Thr Phe
3130	3135	3140	
acc aac	ctg gcc gtc cag ctg	gtg agg atg atg gaa	ggg gaa gga
9570			
Thr Asn	Leu Ala Val Gln Leu	Val Arg Met Met Glu	Gly Glu Gly
3145	3150	3155	
gtg att	ggc cca gat gat gtg	gag aaa ctc aca aaa	ggg aaa gga
9615			
Val Ile	Gly Pro Asp Asp Val	Glu Lys Leu Thr Lys	Gly Lys Gly
3160	3165	3170	
ccc aaa	gtc agg acc tgg ctg	ttt gag aat ggg gaa	gaa aga ctc
9660			
Pro Lys	Val Arg Thr Trp Leu	Phe Glu Asn Gly Glu	Glu Arg Leu
3175	3180	3185	
agc cgc	atg gct gtc agt gga	gat gac tgt gtg gta	aag ccc ctg
9705			
Ser Arg	Met Ala Val Ser Gly	Asp Asp Cys Val Val	Lys Pro Leu
3190	3195	3200	
gac gat	cgc ttt gcc acc tcg	ctc cac ttc ctc aat	gct atg tca
9750			
Asp Asp	Arg Phe Ala Thr Ser	Leu His Phe Leu Asn	Ala Met Ser
3205	3210	3215	
aag gtt	cgc aaa gac atc caa	gag tgg aaa ccg tca	act gga tgg
9795			
Lys Val	Arg Lys Asp Ile Gln	Glu Trp Lys Pro Ser	Thr Gly Trp
3220	3225	3230	
tat gat	tgg cag cag gtt cca	ttt tgc tca aac cat	ttc act gaa
9840			
Tyr Asp	Trp Gln Gln Val Pro	Phe Cys Ser Asn His	Phe Thr Glu
3235	3240	3245	
ttg atc	atg aaa gat gga aga	aca ctg gtg gtt cca	tgc cga gga
9885			
Leu Ile	Met Lys Asp Gly Arg	Thr Leu Val Val Pro	Cys Arg Gly
3250	3255	3260	
cag gat	gaa ttg gta ggc aga	gct cgc ata tct cca	ggg gcc gga
9930			
Gln Asp	Glu Leu Val Gly Arg	Ala Arg Ile Ser Pro	Gly Ala Gly
3265	3270	3275	
tgg aac	gtc cgc gac act gct	tgt ctg gct aag tct	tat gcc cag
9975			
Trp Asn	Val Arg Asp Thr Ala	Cys Leu Ala Lys Ser	Tyr Ala Gln
3280	3285	3290	

atg tgg ctg ctt ctg tac ttc cac aga aga gac ctg cgg ctc atg
10020

Met Trp Leu Leu Leu Tyr Phe His Arg Arg Asp Leu Arg Leu Met
3295 3300 3305

gcc aac gcc att tgc tcc gct gtc cct gtg aat tgg gtc cct acc
10065

Ala Asn Ala Ile Cys Ser Ala Val Pro Val Asn Trp Val Pro Thr
3310 3315 3320

gga aga acc acg tgg tcc atc cat gca gga gga gag tgg atg aca
10110

Gly Arg Thr Thr Trp Ser Ile His Ala Gly Gly Glu Trp Met Thr
3325 3330 3335

aca gag gac atg ttg gag gtc tgg aac cgt gtt tgg ata gag gag
10155

Thr Glu Asp Met Leu Glu Val Trp Asn Arg Val Trp Ile Glu Glu
3340 3345 3350

aat gaa tgg atg gaa gac aaa acc cca gtg gag aaa tgg agt gac
10200

Asn Glu Trp Met Glu Asp Lys Thr Pro Val Glu Lys Trp Ser Asp
3355 3360 3365

gtc cca tat tca gga aaa cga gag gac atc tgg tgt ggc agc ctg
10245

Val Pro Tyr Ser Gly Lys Arg Glu Asp Ile Trp Cys Gly Ser Leu
3370 3375 3380

att ggc aca aga gcc cga gcc acg tgg gca gaa aac atc cag gtg
10290

Ile Gly Thr Arg Ala Arg Ala Thr Trp Ala Glu Asn Ile Gln Val
3385 3390 3395

gct atc aac caa gtc aga gca atc atc gga gat gag aag tat gtg
10335

Ala Ile Asn Gln Val Arg Ala Ile Ile Gly Asp Glu Lys Tyr Val
3400 3405 3410

gat tac atg agt tca cta aag aga tat gaa gac aca act ttg gtt
10380

Asp Tyr Met Ser Ser Leu Lys Arg Tyr Glu Asp Thr Thr Leu Val
3415 3420 3425

gag gac aca gta ctg tag atattttaatc aattgtaaata agacaatata
10428

Glu Asp Thr Val Leu
3430

agtatgcata aaagtgtagt tttatagtag tatttagtgg tgtagtgta aatagttaag
10488

aaaattttga ggagaaagtc aggccgggaa gttcccgcc cccaagtgt agtagacggt
10548

gctgcctgcg actcaacccc aggaggactg ggtgaacaaa gccgcgaagt gatccatgta
10608

agccctcaga accgtctcgg aaggaggacc ccacatgttg taacttcaaa gcccaatgtc
10668

agaccacgct acggcgtgct actctgcgga gagtgcagtc tgcgatagtg cccagagggt
10728

actgggttaa caaaggcaaa ccaacgcccc acgcggccct agccccggta atggtgttaa
10788

ccagggcgaa aggactagag gttagaggag accccgcggt ttaaagtgca cggcccagcc
10848

tgactgaagc tgtaggtcag ggaaggact agaggtagt ggagaccccg tgccacaaaa
10908

caccacaaca aaacagcata ttgacacctg ggatagacta ggagatcttc tgctctgcac
10968

aaccagccac acggcacagt gcgccgacaa tgggtggctgg tgggtgcgaga acacaggatc
11028

t
11029

Figure 13, 5kb C5 locus and PCR primers to amplify C5 arms (SEQ ID NO: 77)

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CTGAAATTGTAATTTCTACATGTAGAGAAGGTTTTGATATTGATGGTTTTAACAGAAACG
GACTTTAACATTAAAGATGTACATCTCTTCCAAAACATAAATACTACCAAATTTGTCTTTGC
      10              20              30              40              50              60

TAGAAATTATATCAAGGGATAACATTTTATATGATATAGTTTTTAAAGTGTAAGATGGAAT
ATCTTTAATATAGTTCCCTATTGTAAAAATATACTATATCAAAAATTTACATTCTACCTTA
      70              80              90              100             110             120

TAAATTTTCATGTGCACAAGAGGCATAGGAGATAAAAGCATTTTCAGACTTTGTATAATGA
ATTTAAAGTACACGTGTTCTCCGTATCCTCTATTTTCGTAAAAGTCTGAAACATATTACT
      130             140             150             160             170             180

AGGAATATGATCAAATAAACAGAATCTGTTAGTTAGTTACTTGGATAAATTAATCGAGA
TCCTTATACTAGTTTATTTGTTCTTAGACAATCAATCAATGAACCTATTTAATTAGCTCT
      190             200             210             220             230             240

CGCGTGATAAAATGACTATGTACCGTTATTGCATGAACGATATTATAAATATAGGTTCTC
GCGCACTATTTTACTGATACATGGCAATAACGTACTTGCTATAAATATTTATATCCAAGAG
      250             260             270             280             290             300

      (C5A1)   GGCCGAATTC
G TAGGAGAGA A C T A T T G A C T A T G G C A A T G A A T G T T A A A T G T T A C T T T G G A T G A A G C T A
C A T C C T C T C T T G A T A A C T G A T A C C G T T A C T T A C A A T T T A C A A T A T G A A A C C T A C T T C G A T
      310             320             330             340             350             360

TAAATATGCATTGGAAAAATAATCCATTTAAAGAAAGGATTCAAATACTACAAAACCTAA
ATTTATACGTAAACCTTTTTTATTAGGTAAATTTCTTTCCTAAGTTTATGATGTTTTGGATT
      370             380             390             400             410             420

GCGATAATATGTTAACTAAGCTTATTCTTAACGACGCTTTAAATATACACAAATAAACAT
CGCTATTATACAATTGATTCGAATAAGAATTGCTGCGAAATTTATATGTGTTTATTGTA
      430             440             450             460             470             480

AATTTTTGTATAACCTAACAAATAACTAAAACATAAAAAATAATAAAAGGAAATGTAATAT
TTAAAAACATATTGGATTGTTTATTGATTTTGTATTTTATTATTTTCTTTACATTATA
      490             500             510             520             530             540

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CGTAATTATTTTACTCAGGAATGGGGTTAAATATTTATATCACGTGTATATCTATACTGT
GCATTAATAAAATGAGTCCTTACCCCAATTTATAAATATAGTGCACATATAGATATGACA
550 560 570 580 590 600

TATCGTATACTCTTTACAATTACTATTACGAATATGCAAGAGATAATAAGATTACGTATT
ATAGCATATGAGAAAATGTTAATGATAATGCTTATACGTTCTCTATTATTCTAATGCATAA
610 620 630 640 650 660

TAAGAGAATCTTGTCATGATAATTGGGTACGACATAGTGATAAATGCTATTTTCGCATCGT
ATTCTCTTAGAACAGTACTATTAACCCATGCTGTATCACTATTTACGATAAAGCGTAGCA
670 680 690 700 710 720

TACATAAAGTCAGTTGGAAAGATGGATTTGACAGATGTAACCTTAATAGGTGCAAAAATGT
ATGTATTTTCAGTCAACCTTTCTACCTAACTGTCTACATTGAATTATCCACGTTTTTTACA
730 740 750 760 770 780

TAAATAACAGCATTCTATCGGAAGATAGGATACCAGTTATATTATACAAAAATCACTGGT
ATTTATTGTCGTAAGATAGCCTTCTATCCTATGGTCAATATAAATATGTTTTTTAGTGACCA
790 800 810 820 830 840

TGGATAAAACAGATTCTGCAATATTCGTAAAAGATGAAGATTACTGCGAATTTGTAAACT
ACCTATTTTGTCTAAGACGTTATAAGCATTTTCTACTTCTAATGACGCTTAAACATTTGA
850 860 870 880 890 900

ATGACAATAAAAAGCCATTTATCTCAACGACATCGTGTAATTCTTCCATGTTTTATGTAT
TACTGTTATTTTTTCGGTAAATAGAGTTGCTGTAGCACATTAAGAAGGTACAAAATACATA
910 920 930 940 950 960

GTGTTTCAGATATTATGAGATTACTATAAACTTTTTGTATACTTATATTCGTAAACTAT
CACAAAGTCTATAAATACTCTAATGATATTTGAAAAACATATGAATATAAGGCATTTGATA
970 980 990 1000 1010 1020

ATTAATCATGAAGAAAATGAAAAAGTATAGAAGCTGTTACGAGCGGTTGTTGAAAACAA
TAATTAGTACTTCTTTTACTTTTTTCATATCTTCGACAAGTGCTCGCCAACAACCTTTTGT
1030 1040 1050 1060 1070 1080

CAAAATTATACATTCAAGATGGCTTACATATACGTCTGTGAGGCTATCATGGATAATGAC
GTTTTAATATGTAAGTTCTACCGAATGTATATGCAGACACTCCGATAGTACCTATTACTG
1090 1100 1110 1120 1130 1140

AATGCATCTCTAAATAGGTTTTTGGACAATGGATTTCGACCCTAACACGGAATATGGTACT
TTACGTAGAGATTTATCCAAAAACCTGTTACCTAAGCTGGGATTGTGCCTTATACCATGA
1150 1160 1170 1180 1190 1200

CTACAATCTCCTCTTGAAATGGCTGTAATGTTCAAGAATACCGAGGCTATAAAAAATCTTG
GATGTTAGAGGAGAACTTTACCGACATTACAAGTTCTTATGGCTCCGATATTTTTTAGAAC
1210 1220 1230 1240 1250 1260

ATGAGGTATGGAGCTAAACCTGTAGTTACTGAATGCACAACCTTCTTGCTCTGCATGATGCG
TACTCCATACCTCGATTTGGACATCAATGACTTACGTGTTGAAGAACAGACGTACTACGC
1270 1280 1290 1300 1310 1320

GTGTTGAGAGACGACTACAAAATAGTGAAAGATCTGTTGAAGAATAACTATGTAAACAAT
CACAACTCTCTGCTGATGTTTTATCACTTTCTAGACAACCTTCTTATTGATACATTTGTTA
1330 1340 1350 1360 1370 1380

GTTCTTTACAGCGGAGGCTTTACTCCTTTGTGTTTGGCAGCTTACCTTAACAAAGTTAAT
CAAGAAATGTGCGCTCCGAAATGAGGAAACACAAACCGTCGAATGGAATTGTTTTCAATTA
1390 1400 1410 1420 1430 1440

TTGGTTAAACTTCTATTGGCTCATTTCGGCGGATGTAGATATTTCAAACACGGATCGGTTA
AACCAATTTGAAGATAACCGAGTAAGCCGCCTACATCTATAAAGTTTGTGCCTAGCCAAT
1450 1460 1470 1480 1490 1500

ACTCCTCTACATATAGCCGTATCAAATAAAAAATTTAACAATGGTTAAACTTCTATTGAAC
TGAGGAGATGTATATCGGCATAGTTTTATTTTTAAATTGTTACCAATTTGAAGATAACTTG
1510 1520 1530 1540 1550 1560

AAAGGTGCTGATACTGACTTGCTGGATAACATGGGACGTACTCCTTTAATGATCGCTGTA
TTTCACGACTATGACTGAACGACCTATTGTACCCTGCATGAGGAAATTACTAGCGACAT
1570 1580 1590 1600 1610 1620

CAATCTGGAAATATTGAAATATGTAGCACACTACTTAAAAAAAATAAAATGTCCAGAACT
GTTAGACCTTTATAACTTTATACATCGTGTGATGAATTTTTTTTATTTTACAGGTCTTGA
1630 1640 1650 1660 1670 1680

GGGAAAAATTGATCTTGCCAGCTGTAATTCATGGTAGAAAAGAAGTGCTCAGGCTACTTT
CCCTTTTTTAACTAGAACGGTCGACATTAAGTACCATCTTTTCTTCACGAGTCCGATGAAA
1690 1700 1710 1720 1730 1740

TCAACAAAGGAGCAGATGTAAACTACATCTTTGAAAGAAATGGAAAATCATATACTGTTT
AGTTGTTTTCCTCGTCTACATTTGATGTAGAACTTTCTTTACCTTTTAGTATATGACAAA
1750 1760 1770 1780 1790 1800

TGGAATTGATTAAAGAAAGTTACTCTGAGACACAAAAGAGGTAGCTGAAGTGGTACTCTC
ACCTTAACTAATTTCTTTCAATGAGACTCTGTGTTTTCTCCATCGACTTCACCATGAGAG
1810 1820 1830 1840 1850 1860

CS ORF

MET GLN ASN ASP ASP CYS GLU ALA ARG SER ARG GLU ILE THR LEU TYR ASP PHE LEU
AAAATGCAGAACGATGACTGCGAAGCAAGAAGTAGAGAAATAACACTTTTATGACTTTCTT
TTTTACGTCTTGCTACTGACGCTTCGTTCTTCATCTCTTTATTGTGAAATACTGAAAGAA
1870 1880 1890 1900 1910 1920
CCATGCACTGATTAATCGATATTTTTTCCATGGGCCC (C5B1)

SER CYS ARG LYS ASP ARG ASP ILE MET MET VAL ILE ASN ASN SER ASP ILE ALA SER LYS
AGTTGTAGAAAAGATAGAGATATAATGATGGTCATAAATAACTCTGATATTGCAAGTAAA
TCAACATCTTTTCTATCTCTATATTACTACCAGTATTTATTGAGACTATAACGTTTCATTT
1930 1940 1950 1960 1970 1980

CYS ASN ASN LYS LEU ASP LEU PHE LYS ARG ILE VAL LYS ASN ARG LYS LYS GLU LEU ILE
TGCAATAATAAGTTAGATTTATTTAAAAGGATAGTTAAAATAAGAAAAAGAGTTAATT
ACGTTATTATTCAATCTAAATAAATTTTCTATCAATTTTATCTTTTTTTCTCAATTAA
1990 2000 2010 2020 2030 2040

CYS ARG VAL LYS ILE ILE HIS LYS ILE LEU LYS PHE ILE ASN THR HIS ASN ASN LYS ASN
TGTAGGGTTAAAATAATACATAAGATCTTAAAATTTATAAATACGCATAATAATAAAAAAT
ACATCCCAATTTTATTATGTATTCTAGAATTTTAAATATTTATGCGTATTATTATTTTAA
2050 2060 2070 2080 2090 2100

(C5C1) GGATCCGGGTTTTTATGACTAGTTAATCACGGCCC

ARG LEU TYR LEU LEU PRO SER GLU ILE LYS PHE LYS ILE PHE THR TYR LEU THR TYR LYS
AGATTATACTTATTACCTTCAGAGATAAAATTTAAGATATTTACTTATTTAACTTATAAA
TCTAATATGAATAATGGAAGTCTCTATTTTAAATTCTATAAATGAATAAATTGAATATTT
2110 2120 2130 2140 2150 2160

ASP LEU LYS CYS ILE ILE SER LYS ***
GATCTAAAATGCATAAATTTCTAAATAATGAAAAAAGTACATCATGAGCAACGCGTTAGT
CTAGATTTTACGTATTAAAGATTTATTACTTTTTTTTCATGTAGTACTCGTTGCGCAATCA
2170 2180 2190 2200 2210 2220

ATATTTTACAATGGAGATTAAACGCTCTATACCGTTCTATGTTTATTGATTCAGATGATGT
TATAAAATGTTACCTCTAATTGCGAGATATGGCAAGATACAAATAACTAAGTCTACTACA
2230 2240 2250 2260 2270 2280

TTTAGAAAAGAAAAGTTATTGAATATGAAAACCTTTAATGAAGATGAAGATGACGACGATGA
AAATCTTTTCTTTCAATAACTTATACTTTTGAAATTACTTCTACTTCTACTGCTGCTACT
2290 2300 2310 2320 2330 2340

TTATTGTTGTAAATCTGTTTTAGATGAAGAAGATGACGCGCTAAAGTATACTATGGTTAC
AATAACAACATTTAGACAAAATCTACTTCTTCTACTGCGCGATTTTCATATGATACCAATG
2350 2360 2370 2380 2390 2400

AAAGTATAAGTCTATACTACTAATGGCGACTTGTGCAAGAAGGTATAGTATAGTGAAAAT
TTTCATATTCAGATATGATGATTACCGCTGAACACGTTCTTCCATATCATATCACTTTTA
2410 2420 2430 2440 2450 2460

GTTGTTAGATTATGATTATGAAAAACCAAATAAATCAGATCCATATCTAAAGGTATCTCC
CAACAATCTAATACTAATACTTTTTGGTTTATTTAGTCTAGGTATAGATTTCCATAGAGG
2470 2480 2490 2500 2510 2520

TTTGCACATAAATTCATCTATTCCTAGTTTAGAATACTTTTTCATTATATTTGTTTACAGC
AAACGTGTATTAAAGTAGATAAGGATCAAATCTTATGAAAAGTAATATAAACAATGTCTG
2530 2540 2550 2560 2570 2580
GACGTCGG (C5D1)

TGAAGACGAAAAAATATATCGATAATAGAAGATTATGTTAACTCTGCTAATAAGATGAA
ACTTCTGCTTTTTTTATATAGCTATTATCTTCTAATAACAATTGAGACGATTATTCTACTT
2590 2600 2610 2620 2630 2640

ATTGAATGAGTCTGTGATAATAGCTATAATCAGAGAAGTTCTAAAAGGAAATAAAAAATCT
TAACCTACTCAGACACTATTATCGATATTAGTCTCTTCAAGATTTTCCTTTATTTTTTAGA
2650 2660 2670 2680 2690 2700

AACTGATCAGGATATAAAAACATTGGCTGATGAAATCAACAAGGAGGAACTGAATATAGC
TTGACTAGTCCTATATTTTTTGTAACCGACTACTTTAGTTGTTTCCTCCTTGACTTATATCG
2710 2720 2730 2740 2750 2760

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ATTTGATAACAATCTATCTCCCGGTTTCATTTAATGTTTCCTACAAATGCCAAGAAGTCG
2770 2780 2790 2800 2810 2820

TCTCCATAGAGCTGCTATTGGTAGGAAACAGGATATGATAAAGCTGTTAATCGATCATGG
AGAGGTATCTCGACGATAACCATCCTTTGTCCTATACTATTTTCGACAATTAGCTAGTACC
2830 2840 2850 2860 2870 2880

AGCTGATGTAAACTCTTTAACTATTGCTAAAGATAATCTTATTAAAAAAAATAATATCA
TCGACTACATTTGAGAAATTGATAACGATTTCTATTAGAATAATTTTTTTTTTATTATAGT
2890 2900 2910 2920 2930 2940

CGTTTAGTAATATTTAAATATATTAATAACTCTATTACTAATAACTCCAGTGGATATGAA
GCAAATCATTATAATTTTATATAATTATTGAGATAATGATTATTGAGGTCACCTATACTT
2950 2960 2970 2980 2990 3000

CATAATACGAAGTTTATACATTCTCATCAAAATCTTATTGACATCAAGTTAGATTGTGAA
GTATTATGCTTCAAATATGTAAGAGTAGTTTTTAGAATAACTGTAGTTCAATCTAACACTT
3010 3020 3030 3040 3050 3060

AATGAGATTATGAAATTAAGGAATACAAAAATAGGATGTAAGAACTTACTAGAATGTTTT
TACTCTAATACTTTAATTCTTATGTTTTTATCCTACATTCTTGAATGATCTTACAAAA
3070 3080 3090 3100 3110 3120

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TAGTTATTACTATACTTATGTCATAGATCCCGATATTTGTTACTTTGCTAATTTTTTAATA
3130 3140 3150 3160 3170 3180

AAAAATCATTTCCCTATATATAATACGCTCATAGAAAAATTCATTTCTGAAAGTATACTA
TTTTTAGTAAAGGGATATATATTATGCGAGTATCTTTTTAAGTAAAGACTTTCATATGAT
3190 3200 3210 3220 3230 3240

AGACACGAATTATTGGATGGAGTTATAAATTCTTTTCAAGGATTCAATAATAAATTGCCT
TCTGTGCTTAATAACCTACCTCAATATTTAAGAAAAGTTCTTAAGTTATTATTTAACGGA
3250 3260 3270 3280 3290 3300

TACGAGATTTCAGTACATTATACTGGAGAATCTTAATAACCATGAACTAAAAAAAATTTTA
ATGCTCTAAGTCATGTAATATGACCTCTTAGAATTATTGGTACTTGATTTTTTTTTTAAAT
3310 3320 3330 3340 3350 3360

GATAATATACATTAAAAAGGTAAATAGATCATCTGTTATTATAAGCAAAGATGCTTGTTG
CTATTATATGTAATTTTTTCCATTTATCTAGTAGACAATAATATTCGTTTCTACGAACAAC
3370 3380 3390 3400 3410 3420

CCAATAATATACAACAGGTATTTGTTTTTATTTTTAACTACATATTTGATGTTTCTTCTC
GGTTATTATATGTTGTCCATAAACAAAAATAAAAAATTGATGTATAAACTACAAGTAAGAG
3430 3440 3450 3460 3470 3480

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AAATATATATCATATGTGTCTTTTAAGTATTAGGTGAATCTTAAAGATCAATAGATCAAAAA
3490 3500 3510 3520 3530 3540

CTAGAATATTGTACTTTATTTCTAATGGAATGGCTCTCCAGCCTAGTAATTTATTAATGT
GATCTTATAACATGAAATAAAGATTACCTTACCGAGAGGTTCGGATCATTAAATAATTACA
3550 3560 3570 3580 3590 3600

TAGCTGATATCTTGAAATCAGGATATTCTGCTCCGTGAAGAGAAAAGTCCTCCAAAGTTGT
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3610 3620 3630 3640 3650 3660

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3670 3680 3690 3700 3710 3720

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3730 3740 3750 3760 3770 3780

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AATTCCGTGTTTAGATTGTACCTTACAGATGGTATTGGGTATTCCAAAAAAGTAAAGGA
3790 3800 3810 3820 3830 3840

CTATCTCTAATACACACTGTTCTTTCCAGACTTTCAACACGCTGCTATTTTCTATTTTAT
GATAGAGATTATGTGTGACAAGAAAGGTCTGAAAGTTGTGCGACGATAAAAGATAAAATA
3850 3860 3870 3880 3890 3900

TCAAGTCCATATTATAAGCGTCCTTGTTAGACACTTCATAATGTTTGCAATCTGGAATCA
AGTTCAGGTATAATATTCGCAGGAACAATCTGTGAAGTATTACAAACGTAAGACCTTAGT
3910 3920 3930 3940 3950 3960

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AGTACAATCTATGATAATTAAATCGATGAAGATACAACAGTAGTTTTCTCAACGATAGAC
3970 3980 3990 4000 4010 4020

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ATTAATGTGATTCTCCACATAGTGGACTATTTCTTCATTATCTCTGTAGACGAGACTTAA
4030 4040 4050 4060 4070 4080

T A A G C A A T A C C T C A A T A A C T T C T T T T G A A G A T G A C T T T G C A G C T A A A A A T A A T G G A G T T C
A T T C G T T A T G G A G T T A T T G A A G A A A C T T C T A C T G A A A C G T C G A T T T T T A T T A C C T C A A G
4090 4100 4110 4120 4130 4140

T C T C T A A A A C A T C C C T T G A G T T T A T A T T A G C C C C G T A A C T A A T G A G T A G T T C T G T T A T A T
A G A G A T T T T G T A G G G A A C T C A A A T A T A A T C G G G G C A T T G A T T A C T C A T C A A G A C A A T A T A
4150 4160 4170 4180 4190 4200

C T T T G G A A T C T A T T G A T A T A T T A T T A A T T A C A A T T G T C A T G C T G A C A T A T A T A G A C A T C A
G A A A C C T T A G A T A A C T A T A T A A T A A T T A A T G T T A A C A G T A C G A C T G T A T A T A T C T G T A G T
4210 4220 4230 4240 4250 4260

T A A T A T G A T G A A A A A T A T G A A A A T A T A A G T G C A C G T T T A C T G T T A C T A T G A T T G T G A T A T
A T T A T A C T A C T T T T T A T A C T T T T A T A T T C A C G T G C A A A T G A C A A T G A T A C T A A C A C T A T A
4270 4280 4290 4300 4310 4320

C G A T A T G A G T T C T T T A A T A A A A G T A C T G A A A T A G A T A T A A T G C A G A T A T G A T T G A T A T T T
G C T A T A C T C A A G A A A T T A T T T T C A T G A C T T T A T C T A T A T T A C G T C T A T A C T A A C T A T A A A
4330 4340 4350 4360 4370 4380

T A A A A A G T T G A A A A A A A A T A T G C C C T G T T T A C A A A T A C T A T T T G G A A A T A T T C T G T A A T A
A T T T T T C A A C T T T T T T T A T A C G G G A C A A A T G T T T A T G A T A A A C C T T T A T A A G A C A T T A T
4390 4400 4410 4420 4430 4440

A A G T A A T A G T G A T A T G T C A G T C A C G A T G G A T T T G C C A A T T G A T C A T A T G A G T A T A G A T A A
T T C A T T A T C A C T A T A C A G T C A G T G C T A C C T A A A C G G T T A A C T A G T A T A C T C A T A T C T A T T
4450 4460 4470 4480 4490 4500

C A T A A A C G A G T A T A A T A A A A A T G G A T A T A C T A G A C T C T A T A T A G A G G T A G C C A T G A A A A A
G T A T T T G C T C A T A T T A T T T T T A C C T A T A T G A T C T G A G A T A T A T C T C C A T C G G T A C T T T T T
4510 4520 4530 4540 4550 4560

A C G T A A A A A C G T A G A T A G A C T T T T A T A T C T C G G A G C T G A T C C G A A T C T G G C T A G T G T A G A
T G C A T T T T T G C A T C T A T C T G A A A A T A T A G A G C C T C G A C T A G G C T T A G A C C G A T C A C A T C T
4570 4580 4590 4600 4610 4620

T T C G T A T T G T C C T C T T C A T A T T G C T G T T A G G A A T G G T A G T T T A A A G A T A A T A A G A T C A T T
A A G C A T A A C A G G A G A A G T A T A A C G A C A A T C C T T A C C A T C A A A T T T C T A T T A T T C T A G T A A
4630 4640 4650 4660 4670 4680

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4690 4700 4710 4720 4730 4740

GGCTATATCATTAGGTAATTATACAGCATGTAAACACTTCTAGATAACAACGCCGATCC
CCGATATAGTAATCCATTAATATGTCGTACATTTTGTGAAGATCTATTGTTGCGGCTAGG
4750 4760 4770 4780 4790 4800

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ATTAATACAATTGATAATGCCATATCAAGGCGAATAATCTCGTTAATATACACTTTTCGG
4810 4820 4830 4840 4850 4860

TGACATAGTTAGACTGCTATTAGATAGAGGAGCTAATTGCAACCACTTAATTACAAAAA
ACTGTATCAATCTGACGATAATCTATCTCCTCGATTAAAGTTGGTGAATTAATGTTTTTT
4870 4880 4890 4900 4910 4920

CGGTAGAACCTATACTGCTTTAGAGAGTCTTAGGAATTGCTTTTTTTAAAGACAATTCTTC
GCCATCTTGGATATGACGAAATCTCTCAGAATCCTTAACGAAAAAATTTCTGTTAAGAAG
4930 4940 4950 4960 4970 4980

ATCATTGTCGATACTAATAT
TAGTAACAGCTATGATTATA
4990 5000

Figure 14. VQH6 amplified fragment (SEQ ID NO:76)

VQ marker

BamH I V I R Q G E N E T
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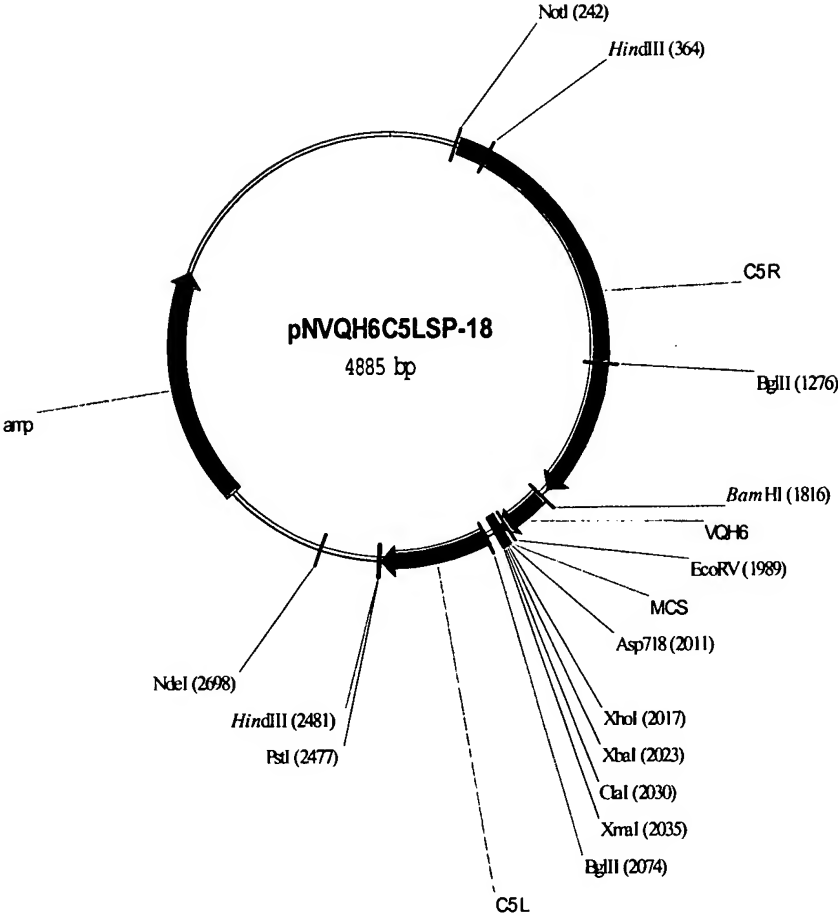
I C S * * * ⇒ H6p
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TAGACGAGCAATTAATTAATCTCGAAGAAATAAGATATGAATTTTTCACT

AAATAAATACAAAGGTTCTTGAGGGTTGTGTAAATTGAAAGCGAGAAAT
TTTATTTATGTTTCCAAGAACTCCCAACACAATTTAACTTTCACCTCTTTA

EcoR V
AATCATAAATTATTTTCATTATCGC GATATC CGTTAAGTTTGTATCGTAGG
TTAGTATTTAATAAAGTAATAGCGCTATAGGCAATTCAAACATAGCAT CC

Kpn I Xho I Xba I Cla I Sma I
TACC CTCGAG TCTAGA ATCGAT CCCGGGTTTT
ATGG GAGCTC AGATCT TAGCTA GGGCCC AAAA

Figure 15. Restriction map of pNVQH6C5LSP-18



Viremia following challenge (data depict plaque-forming units per ml of serum)													
Study Day	Date	DPC	AA349	AA350	AA351	AA356	AA357	AA358	AA359	AA361	AA362	AA363	AA364
26.0	2003-9-16	AM	0.0	0	0	0	0	0	0	0	0	0	0
26.5	2003-9-16	PM	0.5	0	0	0	0	0	0	0	0	0	0
27.0	2003-9-17	AM	1.0	0	0	0	0	0	0	0	0	0	0
27.5	2003-9-17	PM	1.5	0	0	0	0	0	0	0	0	10	0
28.0	2003-9-18	AM	2.0	0	0	0	0	0	0	0	0	0	0
28.5	2003-9-18	PM	2.5	0	0	0	0	5	5	0	0	0	0
29.0	2003-9-19	AM	3.0	0	0	0	0	0	0	20	30	65	0
29.5	2003-9-19	PM	3.5	0	0	0	10	15	10	65	0	40	0
30.0	2003-9-20	AM	4.0	0	0	0	30	35	25	0	50	55	0
30.5	2003-9-20	PM	4.5	0	0	0	55	145	50	0	0	75	0
31.0	2003-9-21	AM	5.0	0	0	0	40	85	40	0	15	10	0
31.5	2003-9-21	PM	5.5	0	0	0	30	10	35	0	0	0	0
32.0	2003-9-22	AM	6.0	0	0	0	20	30	0	25	0	0	0
32.5	2003-9-22	PM	6.5	0	0	0	0	0	0	0	0	0	0
33.0	2003-9-23	AM	7.0	0	0	0	0	0	0	0	0	0	0
33.5	2003-9-23	PM	7.5	0	0	0	0	0	0	0	0	0	0
34.0	2003-9-24	AM	8.0	0	0	0	0	0	0	0	0	0	0
34.5	2003-9-24	PM	8.5	0	0	0	0	0	0	0	0	0	0
35.0	2003-9-25	AM	9.0	0	0	0	0	0	0	0	0	0	0
35.5	2003-9-25	PM	9.5	0	0	0	0	0	0	0	0	0	0
36.0	2003-9-26	AM	10.0	0	0	0	0	0	0	0	0	0	0
36.5	2003-9-26	PM	10.5	0	0	0	0	0	0	0	0	0	0
37.0	2003-9-27	AM	11.0	0	0	0	0	0	0	0	0	0	0
37.5	2003-9-27	PM	11.5	0	0	0	0	0	0	0	0	0	0
38.0	2003-9-28	AM	12.0	0	0	0	0	0	0	0	0	0	0
38.5	2003-9-28	PM	12.5	0	0	0	0	0	0	0	0	0	0
39.0	2003-9-29	AM	13.0	0	0	0	0	0	0	0	0	0	0
39.5	2003-9-29	PM	13.5	0	0	0	0	0	0	0	0	0	0
40.0	2003-9-30	AM	14.0	0	0	0	0	0	0	0	0	0	0
Note: DPC = days post challenge													

Figure 16

VI Results		Day-Time												
Group Name	ID	26-AM	26-PM	27-AM	27-PM	28-AM	28-PM	29-AM	29-PM	30-AM	30-PM	31-AM	31-PM	32-AM
Test Vaccine	AA349	0	0	0	0	0	0	0	0	0	0	0	0	0
	AA350	0	0	0	0	0	0	0	0	0	0	0	0	0
	AA356	0	0	0	0	0	0	0	0	0	0	0	0	0
	AA361	0	0	0	0	0	0	1	1	0	0	0	0	1
	AA364	0	0	0	0	0	0	0	0	0	0	0	0	0
	AA365	0	0	0	0	0	0	0	0	0	0	0	0	0
	AA370	0	0	0	0	0	0	0	0	0	0	0	0	0
	AA373	0	0	0	0	0	0	0	0	0	0	0	0	0
AA374	0	0	0	0	0	0	0	0	0	0	0	0	0	
Test Vaccine Total		0	0	0	0	0	0	1	1	1	0	0	0	1
Unvaccinated	AA351	0	0	0	0	0	0	0	0	0	0	0	0	0
	AA357	0	0	0	0	0	0	0	0	1	1	1	1	1
	AA358	0	0	0	0	0	1	0	0	1	1	1	1	1
	AA359	0	0	0	0	0	0	1	0	1	1	1	1	0
	AA362	0	0	0	0	0	0	0	1	0	1	0	1	0
	AA363	0	0	0	0	1	0	0	1	1	1	1	0	0
	AA368	0	0	0	0	0	0	0	0	0	0	0	0	0
	AA369	0	0	0	0	0	1	1	1	1	1	1	1	0
AA371	0	0	0	0	0	0	0	0	1	1	1	1	0	
AA372	0	0	0	0	0	1	0	1	0	1	0	0	0	
Unvaccinated Total		0	0	0	0	2	1	4	4	6	8	7	4	2

Figure 17a

03-077: West Nile Virus Vaccine -One Dose Efficacy Study
Mean Rectal Temperature by Group and Day

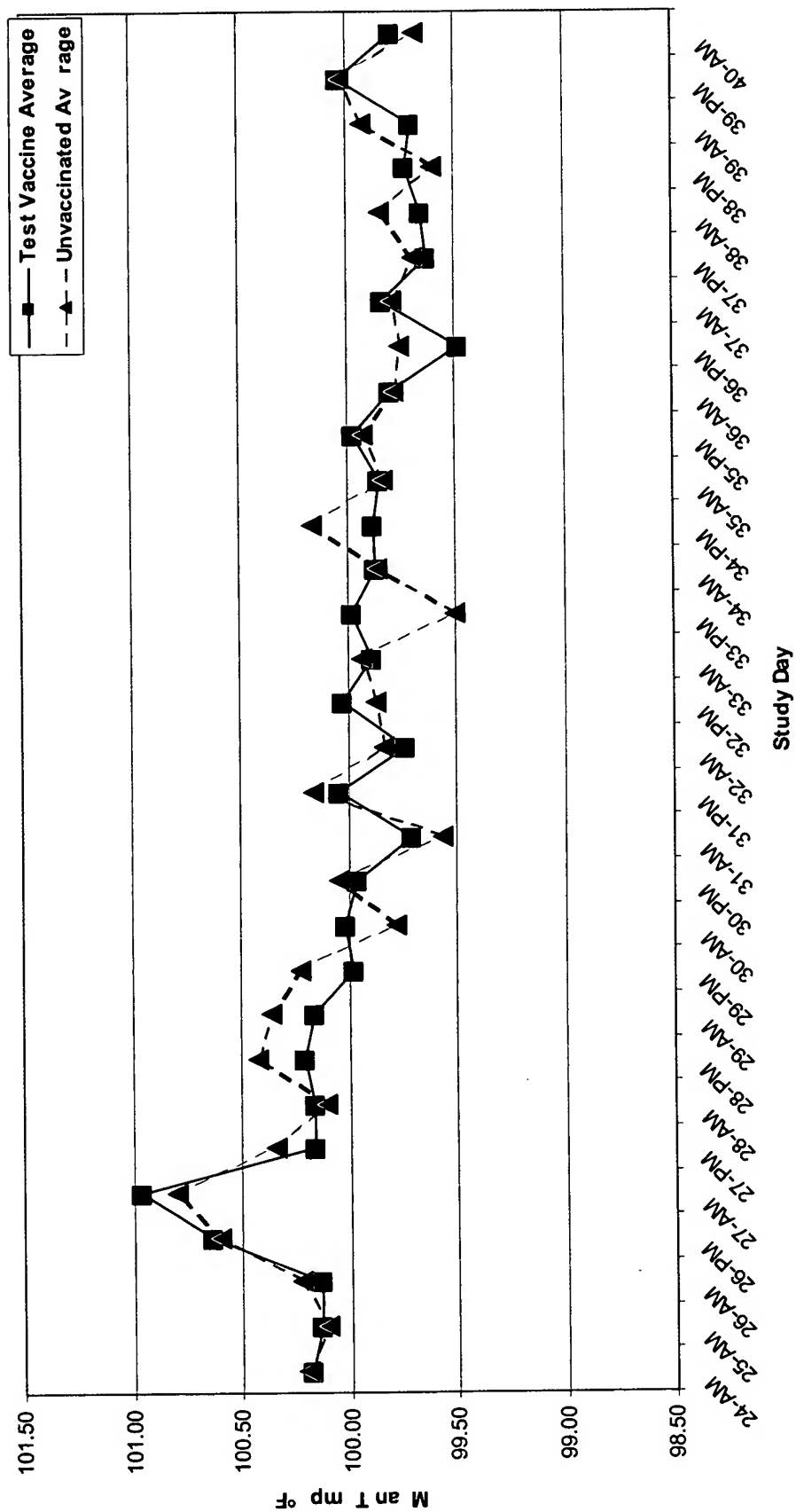


Figure 18c

Plaque reduction neutralization titers													
Study Day	Date	DPC	Reduction	AA349	AA350	AA351	AA356	AA357	AA358	AA359	AA361	AA362	AA363
0	2003-8-21	-26	90%	<5	<5	<5	<5	<5	<5	<5	<5	<5	<5
7	2003-8-28	-19	90%	<5	<5	<5	<5	<5	<5	<5	<5	<5	<5
14	2003-9-4	-12	90%	<5	<5	<5	<5	<5	<5	<5	10	<5	<5
21	2003-9-11	-5	90%	<5	<5	<5	5	<5	<5	<5	10	<5	<5
26	2003-9-16	0	90%	<5	<5	<5	<5	<5	<5	<5	<5	<5	<5
33	2003-9-23	7	90%	40	10	<5	40	<5	<5	<5	10	<5	<5
40	2003-9-30	14	90%	>=160	>=160	40	>=160	>=160	80	>=160	>=160	80	>=160
0	2003-8-21	-26	80%	<5	<5	<5	<5	<5	<5	<5	<5	<5	<5
7	2003-8-28	-19	80%	<5	<5	<5	<5	<5	<5	<5	<5	<5	<5
14	2003-9-4	-12	80%	<5	5	<5	5	<5	<5	<5	10	<5	<5
21	2003-9-11	-5	80%	<5	5	<5	5	<5	<5	<5	20	<5	<5
26	2003-9-16	0	80%	<5	<5	<5	5	<5	<5	<5	5	<5	<5
33	2003-9-23	7	80%	80	20	<5	40	<5	<5	<5	20	<5	<5
40	2003-9-30	14	80%	>=160	>=160	80	>=160	>=160	>=160	>=160	>=160	>=160	>=160
0	2003-8-21	-26	50%	<5	<5	<5	<5	<5	<5	<5	<5	<5	<5
7	2003-8-28	-19	50%	<5	<5	<5	<5	<5	<5	<5	<5	<5	<5
14	2003-9-4	-12	50%	<5	20	<5	10	<5	<5	<5	80	<5	<5
21	2003-9-11	-5	50%	<5	20	<5	20	<5	<5	<5	80	<5	<5
26	2003-9-16	0	50%	<5	5	<5	20	<5	<5	<5	40	<5	<5
33	2003-9-23	7	50%	>=160	80	20	>=160	<5	<5	<5	>=160	<5	5
40	2003-9-30	14	50%	>=160	>=160	>=160	>=160	>=160	>=160	>=160	>=160	>=160	>=160

Figure 19a

Study Day	AA364	AA365	AA368	AA369	AA370	AA371	AA372	AA373	AA374
0	<5	<5	<5	<5	<5	<5	<5	<5	<5
7	<5	<5	<5	<5	<5	<5	<5	<5	<5
14	<5	5	<5	<5	<5	<5	<5	<5	<5
21	<5	<5	<5	<5	<5	<5	<5	<5	<5
26	<5	<5	<5	<5	<5	<5	<5	<5	<5
33	40	5	<5	<5	10	<5	5	10	5
40	80	80	>=160	>=160	>=160	>=160	>=160	>=160	>=160
0	<5	<5	<5	<5	<5	<5	<5	<5	<5
7	<5	<5	<5	<5	<5	<5	<5	<5	<5
14	<5	10	<5	<5	<5	<5	<5	<5	<5
21	<5	<5	<5	<5	<5	<5	<5	<5	<5
26	<5	5	<5	<5	<5	<5	<5	<5	<5
33	80	10	<5	<5	10	<5	5	20	10
40	>=160	>=160	>=160	>=160	>=160	>=160	>=160	>=160	>=160
0	<5	<5	<5	<5	<5	<5	<5	<5	<5
7	<5	<5	<5	<5	<5	<5	<5	<5	<5
14	5	40	<5	<5	<5	<5	<5	10	<5
21	5	10	<5	<5	<5	<5	<5	10	5
26	10	20	<5	<5	5	<5	<5	<5	<5
33	>=160	20	<5	5	40	10	40	80	40
40	>=160	>=160	>=160	>=160	>=160	>=160	>=160	>=160	>=160

Figure 19b